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Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

A;Experimental source: B cell A;Note: the authors translated the codon ACA for residue 13 as Ala 0.8 perfamily: immunaglebulin V region; immunaglebulin hemology C;Keywords, heterotetramer, immunoglobulin

Matches Query Match Best

y Match 100.0%; Score 31; DB 2; Length 21; Local Similarity 50 0%; Prod No 1 30+02; hes 3; Conservative 3; Mismatches 0; Indels

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A; Molecule type: mRNA A; Residues: 1-21 < MCH >

A; Accession: PH1731

SUMMARIES

Result No.	score	Query Match 100.0	Length21	DB	ID 9H1731 148681	Description Ig heavy chain V r
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Ig heavy chain V region (clone GCC-11) - mouse (fragment) C;Species: Mus musculus (house mouse) C;Date: 24 Feb-1994 #sequence_revision 24 Feb 1994 #text_change 17-Mar-1999 C;Accession: PH1731

RESULT 1

P.McHeyzer Williams, M.S., McLean, M.J., Lalor, F.A., Nossal, G.J.V. J. Exp. Med. 178, 295-307, 1993
A.Titlo: Antigen-driven B cell differentiation in vivo.
A.Peference number: PH1675; MUID:93301607; PMID:8315385

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185 kDa glycophosphoprotein - mouse (fragment)
C/Species: Mus musculus (house mouse)
C/Species: Mus musculus (house mouse)
C/Accession: 148681
C/Accession: 148681
R.Withe, M.B.; Hung, M.C.
Oncogene 7, 677-683, 1992
A.Title Cloning and characterization of the mouse may promoter.
A.Peference number 148681, MUD-30008496; PMID:1348855
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C;Keywords: ATP; phosphoprotein
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A;Status: preliminary; translated from GB/EMBL/DDBJ
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C;Genetics:
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A; Residues: 1-49 < RES>
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RiHayashi, T., Makino, Y., Ohnishi, M., Pirrkiwa, Y., Ishii, Y., Tikiyara, Y., Hin, gashwiri, M., Yasunoga, T., Euhara, S., Shika, T., Hatturi, M., Shinagawa, H. DNA Res. 6, 11-22, 2001

Affitle: Complete general engineer of rither dominibagin Escherichic of 157 H7 and Agreference number. Accord, MUID.21156231; FMID.1128936

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A/Experimental southern strik OffT:H7, substrain PIMD 0500000
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A; Residues: 1-61 < HAY>
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E,Wird, D.W., Serthal, T.C., Karl, F., Manks, D., Shen, J., Wied, G.E., Shen, Y., Wied, E,Wird, D.W., Serthal, T.C., Karl, F., Manks, D., Shen, J., Wied, G.E., Shen, Y., Wied, Louge, G., Silet, W., Stand, F., Guencheel, E., Eutyavit, T., Eety, K., M., K., McCella 
Flags, T., Foresto, E., Canag, S., Selecce 204, 2017, 2023, 2001

A,Authors Yes, H., Tas, Y., Fiddio, F., Sing, M., Firspan, W., Surry, M., Gordon-Kamm, I 
A,Authors Yes, H., Tas, Y., Fiddio, F., Sing, M., Firspan, W., Surry, M., Gordon-Kamm, I 
A,Authors (1997)
A, Reference number. AB2017,
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8.NJ, W.Y.; Mannedy, S.E.; Mahairus, G.G.; Retjihst, E.; Dan, M.; Shikis, H.D.; Laught, H.V.; Mannedy, S.E.; Mahairus, B.; Dansin, M.Z.; High, D.W.; Yiditiks, D.C.; Jung, F. H.; Alim, M.; Freitas, T.; Jung, F. H.; Alim, M.; Freitas, T.; Jung, A.C.; And Dan, M.Z.; Jung, A.C.; Jung, A.C.; Bibble, M.Z.; 
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A.TILLe. The primary schedule of the antenna polymetrides of Establishedospica haloshi
A.Fr-F-reit minist. CT3184, MTHF 92147896, EMED 1877899
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A;Residues: 1-71 <STO>
A;Chas references 35
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R:Lindler, L.E.; Plano, G.V.; Burland, V.; Mayhew, G.F.; Bla-Infect. Immun. 66, 5731-5742, 1998
A;Title: Complete DNA sequence and detailed analysis of the A;Reference number: 218268; MHD-99041899; PMID-9826448
A;Accession: T15006
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A;Status: preliminary
A;Molecule type DNA
                        A;Cross-references
C;Genetics
                                                                     A; Molecule type: DNA
A; Residues: 1-78 < REN>
                                                                                                                                                                   R;Renaudin, J.; Aullo, P.; Vignault, J.C.; Bove, J.M.
Nucleic Acids Pes 18, 1993, 1999
A;Title: Complete nucleotide sequence of the genome of Spiroplasma citri virus SpV1-R8A2
A;Reference number: S08447; MIID:00206790; pMID:2320423
                                                                                                                                                                                                                                                                                    hypothetimal protein a spiroplasma virus l
C.Species: spiroplasma virus l, SpVi
C.Date: Wh.Tun-1991 #sequence_revision Wh.Tun-1991 #rext_change 07-Dec-1999
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A; Residues: 1 of FITMS
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A; Residues: 1-76 < HUP>
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A;Accession: T14724
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A;Residues: 1-7% /FUP>
A;Genetic
                                                                                                                     A; Status: translation not shown
                                                                                                                                              A; Accession: S08449
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R;Lindler, L.E.; Plano, G V ; Burland, V ; Mayhew, G F ; Blattner, F P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hypothetical protein Y1091 - Versinia pestis plasmid pMT1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: EMBL:AE074611, MID glasions, DID glasions, DIDM AAC82740-1
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Best Local :
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|Species: Versinia #sempence revision 20 Sep 1999 #*Ext_change 24-Sep-1999
|Accession: T14724; T15006 |
                                                                                                                                                                                                                                                                         Accession: S08449
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oude: 5003
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                                             EMPL: XE1944; MID: GA1900; PIDM CAARSTO 1;
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Pred No 3 9e+02;
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R;Plartner, F.R.; Plunkert III, G.; Rloch, C.A.; Perna, N.T.; F.A.; Rose, D.J.; Mau, B.; Shao, Y. Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12. A;Peforence micher: A64720; MUID: 07426617; PMID: 9278603
A;Accession: A64750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hyporhetical protein h0249 - Escherichia coli (strain K-12)
C;Species: Escherichia coli
C;Becies: Escherichia coli
C;Date: 11-Sep-1997 #seguence_revision 17-Sep-1997 #text_change 01-Mar
C;Accession: A64750
C;Accession:
F;Burland, V
                                         conserved hypothetical protein L7085 - Escherichia coli plasmid p0157
C;Spacies: Escherichia coli
C;Sate 20-Fe;1970 #sequence_revision & Chec 1999 #text_phange 03-Fec-1999
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A; Residues: 1-83 < KUR>
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A;Accession: A97568
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A.; Liu, F., Wollam, C., Allinger, M., Doughty, D., Spott, C., Unppur, C., Mai
Science 294, 2023-2029, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C,Date: 30.Gep.2001 #sequence_revision 30 Sep 2001 #rext_change 11 Jan 2002
C;Accession: A97568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Experimental source: strain F-12, substrain MG1655
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A;Residues: 1-79 <BLAT>
A;Cross:teferences: GR AECOCLE, GB-HONORG, DII 3;797079, TIIN AATTOOLE);
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A)Cross-references: GB:AE007869; PIDM:AAF87498 i) PIDg1818FFFF, GSFFF-GWEG189
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Shao, Y., Ferna, N.I., Flunkerr, G., Sofia,
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50.0%; Pred. No. 4.1e+02;
tive 3; Micmatches 0; Indels
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Fred. N., 4.3e+02;
3, Mismatches 0
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H.J., Blattmer, F.R
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ArClose-references: EMSL:Z18801; MID:g405659; F1DM:CAAs1356.1; F1D:g405660
C:Superfamily. immuneglebulin V region, immuneglebulin homology
C:Keywords: heterotetramer; immuneglebulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A/Accession: H86763
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-87 65703
A/Cross-references: 35.A5005476, iii.gla/23703, iibN.AAK03130.1, d3fbb.dNu0146
A/Experimental source: strain I51403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nucleic Acids Res. 26, 4196-4204, 1998
A)Title: The Complete CNA sequence in Familysis of the large mindered plasmid of Escher A)Reference in Nervice CNA sequences; Multi-Salistival, EMID:Salistival
A)Accession: T42184
A)Charle (Philips), translated is mindered as Seneral CNA
A)Residence, 186 SETE NA
A)Residence, 186 SETE NA
A)Residence, 186 SETE NA
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A; Residues: 1-92 < KLE>
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R;Kiein, U; Kueppers, R.; Pajewsky, K.
submitted to the EMBL Data Library, September 1993

A;Description: Human IgM(+) IgD(+) cells, the major P cell subset in the peripheral blooc
                                                                                                                                                                                                                                                                                                                                                                     Ig Kappa chain V region (V-kappa 3) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 06-Jan-1995 #sequence_revision 06 Jun 1995 #text_change 23 Jul 1997
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A;Accession: $37509
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A;Note: L7085
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                                          Similarity 50.
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                                   100 0%; Shore 31; DB 2; 1
50.0%; Frod. Mo. 4.76+02;
firm 3; Missurches 0;
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A, Title: Sequence analysis of the CDR, SH and G games of tasks; this assection of tasks to the color of tasks; this class to the color of tasks; this assection of tasks the color of tasks; this class the class of tasks; this class of tasks; this assection of tasks; this class of tasks; this assection of tasks; this class of tasks;
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 Database .
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Maximum DB seq length: 260000000
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Perfect score:
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Gapop 10.0 , Gapext 0.5
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution

SUMMARIES

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                                                                                                                                                                                                                                                                                                                                                                                                                                              ACHA_FELCA
P54250;
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Eukaryota, Meraroa, Chordaro, Cramiata, Vertekraro, Elfeleostomi,
Mammalia, Eutheria, Carmivora, Fissipedia, Felidae, Felis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ol-oom-look (Pel 34, Greated)
Ol-oom-look (Pel 34, Greated)
Ol-oom-look (Pel 41, Last segmence update)
Is-unk 2000 (Pel 41, Lost annotation update)
Acetylcholine receptor protein, alpha chain (Fragment)
                                                                                                SEQUENCE
                                                                                                                                                                                                         InterPro; IPR001175; Neur_channel.
Pfam; PF02931; Neur_chan_LBD; 1.
PROSITE; PS00236; MEDP0TF_ION_CHANNEL;
                                                                                                                                                                                                                                                                        entities requires a linense agreement (some send an email to license@isb-sib.ch).
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63 WKHWVF 68
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                      1 WXXWXF 6
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                                                                                                                                                                                                                                                                                                                                                                                                    MUSCLE) CHAINS
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                                                                                                                                                                                              Postsynaptic membrane; Ionic
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                                              Conservative
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J
                                    Fred Mo. 1.7e+12, Identity of the Most 1.7e+12, Momarches 0; Indels
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                                                                                                                                   SIMILARITY)
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ASSOCIATED WITH PECEPTOP ACTIVATION
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1 7=+02;
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Best Local
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16-00T-2001 (Rel. 40, Created)
16-00T-2001 (Rel. 40, Last sequence update)
16-00T-2001 (Pel. 40, Last apporation update)
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Blatther F F., Flinker C. III, Plot. T A., Perra M T., Purland Piloy M., Collado-Viáns J., Glasner T. L., Pode C M., Mayhew G.F., Gregor J., Collado-Viáns J., Glasner T. L., Pode C M., Mayhew G.F., Gregor J., Covis N.W., Kirkpartick H A., Gooden M A., Rose D.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ECOLI
                                                         MEDLINE=97105885; PubMed=8948633; Himmelreich R., Hilbert H., Plagens H., Pirkl E.,
                                                                                                                                                                                                                                                                                             Hypothetical lipoprotein MPN650 precursor (E09_orf101). MPN650 OF MP192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mau B.,
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ენმბ<u>მ</u>5;
   "Complete se
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YG50
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ECOGene; EG13309; YPJ1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright It is produced that the article between the Swiss Institute of Dicinformatics and the EMBL outstands between the Swiss Institute of Dicinformatics and the EMBL outstands between the Swiss Institute of Dicinformatics.
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STRAIN=K12 / MG1655;
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15-JUN-2002 (Rel.
                                                                                                                   SEQUENCE FROM N.A.
STEAIN ATCC 29342 /
                                                                                                                                                                                                                                                            Mycoplasma pneumoniae
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      seguence analysis of the genome of the banterium Mycopilasma
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095178;
095178;
15-UUL-1990 (Rel 38, Treared)
15-UUL-1990 (Rel 38, Last Sequence update)
15-UUL-1990 (Rel 38, Last sequence update)
15-UUL-2002 (Rel. 41, Last annotation update)
18-UUN 2002 (Rel. 38, Last sequence update)
18-UUL-1990 (Rel 38, Treared)
18-UUL-1990 (Rel 38, Treared)
18-UUL-1990 (Rel 38, Treared)
18-UUL-1990 (Rel 38, Last sequence update)
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Pfam; PFO:
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Dlandy Q. E., Ye M., W. X. Y., Fen C. X., Thaw M., Ehaw C.-J., Fu G.,

Shen Y., Fan H.-Y., Lu G., Ehong M., X. X. K., Haw E. J., Chang T. W.,

Thaw J., Huang Q.-H., Zhou J., Hu G.-X., Gu J., Chen S.-J., Chen Z.,

"Cloning and functional analysis of STMAR with spec reading function
300 precipally undefined globs ognessed in CT24+ lengthplietic
etem/progenitor >-11s %
Gundan Russ 10:1546 1576(2000)
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                        TISSUE=Lung;
Strausberg R.;
Submitted [PPC
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Probot, F00032076, Lipoprotein_1, 1.7
PROSSILE, PSONOWAN, PEUMAR LIPOPROTEIN, 1.
Hypophetical protein; lipoprotein; Membrane; Signal,
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TISSUE=Blood,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PPOT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Walker J.E., Arizmendi J.M., Dupuis A., Fearnley I.M., Finel M., Medd S.M., Filkington S.J., Runswick M.J., Skehel J.M.; "Sequences of 20 submits of NABH-shiquenone exidereductase from bowine heart mirechendria Application of a newel strategy for sequencing proteins using the polymerase chain reaction."; J. Mcl. Biol 226 1041 1072(1942).

1. HOTTON: TRANSFER OF ELECTRONS FROM NACH TO THE ENZYME IS RELIGIBLED.

CHAIN THE IMMEDIATE ELECTRON ACCEPTOR FOR THE ENZYME IS RELIGIBLED.
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01-JUL-1993 (Fel. 26, Last sequence update)
15-JUN-2002 (Fel. 41, List annotation update)
HADH ubiquimone exidereductase ACOS schunit, mitochondrial
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S28241; S28241
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Actinopterygii, Heopterygii, Teleostoi; Ostariophysi Ohmo (Opprinidae; Carassius, NCBI_TaxID=70s7.
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01 JAN-1988 (Rel. 06,
01 NOV-1997 (Pel. 35,
       MEDLINE-87260937; PubMed-3037534;
Luddaya F A, Thi L., Misri T F , Silver S.;
"Mublectlide sequence and expression of the mercurial recistance operion from Staphylococcus aureus placmid p1258.";
Proc. Natl Acad sci U.S A 84 Sin6-Silo(1987).
--- FUNCTION INVOLVED IN MERCUREC TRANSPORT PASSES A (FG(2+)) IN
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MEDLINE=88144476; PubMed=3125551;
Wilson M.R., Middleton D., Warr G.W.;
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01-NOV-1990 (Rel
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SMAFT, SM00406; IGv; 1.
Immunoglobulin V region; Signal.
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HSSF; F01772; 2FB4.
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Ty heavy chain V region 5A precursor.
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COMPLEMENTARITY-DETERMINING
FRAMEWORK-3.
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Goldfen R., Carren D.A.,
"Cloning and Cognor determination of a human show still fast
light-chain good",
Proc. Natl. Acad. Coi. U.C.A. 83.2125 [199(1986)]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM M.A.
MEDLINE-86177570; PubMed-3083417;
METHOD P., 8'79' 7, F M.J.S., HA
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01-NOV-1990 (Rel
15-771-1009 (Pel
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InterFic; IFRC0359; Ig.
Pfan; PF00047; ig. 1.
SMART, SM00406; IGV; 1.
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A01898; K3HUCL.
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28 48 POTENTIAL.
71 91 POTENTIAL.
47 47 HG(2+) (POTENTIAL).
48 48 HG(2+) (POTENTIAL).
114 114 HG(2+) (POTENTIAL).
115 115 HG(2+) (FOTENTIAL).
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Catarrhini, Hominidam, Homo
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Johnston M., Andrews S., Brinkman R., Cooper J., Ding H., Dover J.,
Johnston M., Andrews S., Brinkman R., Cooper J., Ding H., Dover J.,
Johnston L., Keisel C., Kirsten J.,
Kroaba T., Hiller L., Johnston L., Langoton Y.,
Latrellie P., Louis E.J., Macri C., Mardis E., Menceen S., Mouser L.,
Khan M., Rifeic L., Eiles L., St Peter B., Tronseki: E., Vauqhan K.,
Vigiadi D., Wilcox L., Wahldman F., Watersten R., Wilson R.,
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RESULT 15 YA91_MYCPN

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Search completed: February 20, 2001, 10:48:02 Job time: 7.66667 secs
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Rest Local Similarity 50.5
Throbbon 7, Conservative
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16-0CT 2001 (Rel. 40, Created)
16-0CT 2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Pel. 40, Last annotation update)
Hyporherical profein MPN091 (R02_orf138).
                                                                                                                                                                                                         EMBL; AE000008; AAB95711.1; -.
Hyporherical protein: Complete proteome.
PSEQUENCE 138 AA; 15763 MW; PS23805428F42709 CRC64;
                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licensewisb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN ATCC 29342 / M129,
MEDLINE-97105885; PuhMed=8948633;
Himmelreich R., Hilbert H., Plagens H., Pirkl E., Li B.-C.,
                                                                                                                                                                                                                                                                                                                                                                                                                            "Complete sequence analysis of the genome of the bacterium Mycoplasma pneumoniae.";
Nucloic Acids Res. 24:4420-4449(1996).
-'- SIMILAPITY: ALMOST ICENTICAL TO M.PHELMONIAAE MEN413 AND MEN463.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution

SUMMARIES

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Wolan E., B.lan Alvard E.,
Submitted (SEP-2001) to the EMBL/SenBank/EDBC databases
EMBL, AR946614, EALLFS10.17 -.
EMBL, AR946614, EALLFS10.17 -.
EMBL, AR946615, EALLFS10.17 -.
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SETRAIN-970316;
Taniquohi Y., Takehsia J., Bikandou B., Mboudjoka I.,
N'Doubli W.Y., M'Endli M., M'Enle E., Harada Y., Hayadi
Indical W.Y., H'Endli M., M'Enle E., Harada Y., Hayadi
Indical R. Farri H.J.,
Patrill Thiyer f. HIV. Type i Buend in the hpurent Suquencos in
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Mesogastyopoda, Nittorinoidea, Littorinidae, Littorina.
NCBI_Taxio-31823)
                                                           263365 PRELIMINARY; PRT; 48 AA. 263365; CTEMBLEEL 01, Created) C1-NOV-1996 (TIEMBLEEL 01, Last sequence up 01-MAR 2002 (TIFMBLEEL 20, Last annotation Transforming oncogene NEU (Fragment). Rattus norvegicus (Rat).
NCBI_TaxID=10116;
                      Eukaryota: Metazca; Chordata; Craniata; Vertebrata; Euteleostomi
Mammalia, Eutheria, Braccia, Orio, gurti, Mucilie, Mucilie, Fa
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Q18615;
Q1-NOV-1996 (TrEMBLrel. 01, Created)
Q1-NOV-1996 (FramBlrel. 01, Last sequence update)
Q1-NOV-1996 (FramBlrel. 01, Last sequence update)
Q1-Li Holl 1099 (FramBlrel. 11, Last sequence update)
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BEQUENCE FROM M.A.
BEDUTHE SIGG1737, Fubbad D103092;
Suen T.C., Hung M.C.;
"Miltigla" in and himse at log alweets
"Miltigla".
                                                                                                                                                                                                                                                                                                                                                                             MEELINE 30008496, P.LMod 1348855; White M.K.-A., Hong M.-C.; "Cluding and Characterinition of the mouse new promoter."; Charactering the first the mouse new promoter."; Charactering ACTIVITY, ATF + A FROTEIN THROSINE - ADF + E TYROSINE PHOSEHATE.
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Transmembrane; Glycoptotein; Doplication, Receptor; Transfer protein kinase, ATP linding, Phophorylation, NON_TER 49 49
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EMBE; M61004; AAA41686.1; -.
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Moi. Celi. E
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MEELINE OCCOSADO, PubMod 1348855;
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M21.3541., EPP.3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=20365717; PubMed=10910347;
Simpson A.T.G., Reinach F.C., Arru
Alvarenga P., Alves L.M.C., Araya
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         by a translocation breakpoint in an autistic individual."; Am. J. Hum. Genet. 67:510-514(2001).
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EMBI, AERONA66, NAF92039.1; -.

InterPro; IPPRO01207; Prenyl_sire

PROSITE; B890294; PRENYLATION, UNKNOWN_1.

Hypothetical protein; Complete proteome

SEQUENCE -9 AA, TOR MW; EEGD7:F:17.77
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SPECIES=E coli 0157·H7; STRAIN=0157·H7 / EDL943 / ATCC 700927;
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                                                        Length 61;
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                                                                                   Query Match
Best Local Similarity 50
Those 3, Corservation
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100 0%; Snore 31; DE 4; Length 64;
Best Local Complatity COLOS, Fred. Mic 6.20002.
Matches 3; Objective 1; Mismarthes 1, 163-1.
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01-MAR-2002
01-MAR-2002
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NON_TER
SEQUENCE
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01 MAR 2001 (TrEMBLrel. 16, Created)
01 MAR 2001 (TIEMBLrel. 16, Last sequence update)
01-JUN 2002 (TrEMBLrel. 21, Last annotation update)
Putative thymidylate cynthase (Flugment).
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NOW TER
NOW TER
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Strausk-ry R
Submitted (DEC-2001) to the EMEL/Jensank/TIST
Submitted (DEC-2001) to the EMEL/Jensank/TIST
BMSL, BCC17733, AAN17733.1,
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01-MAR-2002 (TrEMBIrel 20, Isat sequence update)
01-MAR-2002 (TrEMBIR) 20, Isat sequence update)
01-MAR-2002 (TrEMBIR) 20, Isat sequence)
Hypothotical 7.5 kDa protein (Fragment).
Hemo sapiens (Human)
Feron sapiens (Human)
Full Control of Cardina, Crania, Nettebrat
Manimalia, Eutheria, Frimates: Catannhini, Howlinid
                                                                                                                                                                                                                                                                                                                                                                                                                         Basso A., Campanile C., Ferrara L., Damiani G., "Organization and analysis of DNA fragmonts of thined by rapided amplified polymorphic DNA (FARP) technique from Lactobacilla saked strained.", Submitted (TT 2000) * The EMBL/Organization dualization.
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| Hartobacillaceae, Lactobacillus.
| Non-Talegae
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                                                                                                                                                                                                                                                                        EMER, A.444622, CACCOCAC.1, ...
SCOT, ECC169, ITCH.
Encerpro, IPBRO0398, Thymidylat_cynt.
Pfam, PF00303, thymid, Lat_cynt, 1.
ProDom, PD001190; Thymidylat_cynt; 1.
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     FAWBOW OF
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9499 WK.
                                                                                                                             50.0%;
                                                                           0%; Pred. No. 6.8e+02;
3; Mismatches 0
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Catarrhini, Hominidae, Homo.
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RR NG MAV., Kennedy S.R., Mahairas G.G., Berquist B., Pan M.,

RR NG MAV., Kennedy S.R., Ballya M.S., Thorrow V., Shrogna J.,

RA Shakla H.D., Lakky S.R., Ballya M.S., Thorrow V., Shrogna J.,

RA Swartzell S., Well D., Hall J., Dahl T.A., Welt, H., Goo Y.A.,

RA Swartzell S., Weller K., Cluz B., Lancan, M.J., Hough D.W.,

K. Madillas I. J., Calling F.F., Kith M.J., Angewich M. J. J.,

K. Taenhatger T.A., Feck R.F., Fohlachioder M., Spudich J.L., Jung K.H.,

RA Alam M., Freitas T., Hou S., Daniels C.J., Dennis P.P., Omer A.D.,

RA Bibardt H., Lowe T.M., Lidaly F., Eiley M., Hold I., CasSarma S.,

F. Tech. W. S., Pohlach M. J., CasSarma S.,

F. Dock Matl. Acad. S. M. M., Sarowa M. M. J., CasSarma S.,

MMCL. New S., ANGUSTIA.) ...

MMCL. ABOOST F. ANGUSTIA.) ...

MEDITOR D. LOWER M., MARCHARA C. M. M.,

MEDITOR D. LOWER M., MARCHARA C. M. M.,

MEDITOR D. CKC64,
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Best Local Similarity 50.0
"Those 3; Conservative
                                                                                                                                                                                           Best Local Similarity
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Robison K.;
Sulmitted (SET:1394) to the E
EMBL, U15187; AAA63114.1; -.
EMBL, U45187; AAA6, 8949 MW;
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Q50168;
u1-NQV-1996
01-NOT 1096
01-NOT 1096
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Q9HST8;
Q1-MAR-2001
C1-MAR-2001
C1-MAR-2001
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VNG0079H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CECUENCE FROM M.A.
Smith D.R.;
Submitted (AFF 1898) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Firmioutes, Actinobacteria, Actinobacteridae;
Actinopyriaby, Tayola to look, My bacteria.
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Arobaca, Euryarchaestu, Halobacterium.
Halobacteriuscae, Halobacterium.
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59 WVKWLF 64
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                                                                                  WYXWXF 6
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(Tremblie).
(Tremblie).
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(TrEMBLiel Of List sequence update)
(TreMBLiel Of Last southills update)
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                                                                                                                                                            Pred. No. 7.1e+02;
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RESULT 13

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RA Baker S., Basham D., Bentley S.D., Procks K., Cerdeno-Tatraga A.M. Chillingworth T., Cronin A., Davies P.M., Davis P., Dougan G. RA Feltwell T., Hamlin M., Harryl S., Magdals K.V. RA Leather S., Monile S., Moyson D.C.F., Quail M., Butherford K.V. RA Simmonds M., Skelton J. Stevens K., Whitehead S., Harryl B.G., RT "Genome sequence of Yersinia poatis, the Justice lgac' of glague ", Nature 413.523 527(2001).

DR RMBL, AP053947, AAC132431; -.

DR EMBL, AP054061; AAC82749.1; -.

SMBL, AL117211; CAB55242.1; -.

W Hypothetical protein. Place.
 Q984W3
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Best Local S
Matches
                                                                                                            01-MAY 2000 (TrEMBLrel. 13, Created)
01-MAY 2000 (TrEMBLrel. 13, Last sequence update)
01-MAY 2000 (TrEMBLrel. 13, Last annotation update)
Hypothetical 9.1 kNa protein.
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01-AUG-1998 (TrEMBLrel 07, Last seguence update)
01-MAR-2002 (TrEMBLrel 20, Last annotation update)
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Kobayashi A., Brubaker R.R., Garcia B.;
"Structural organization of virulence-associated plasmids of Yersinia
                                                                                                                                                                                                                                                                                                                                                                                                                        Hypothetical protein; Plasmid; Complete proteome. SEQUENCE 76 AA; RE07 MW; 7FF44417755016PB CP064;
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Hu P., Elliott J., McCt⊬ady P., «
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EMPL: ARROGARS: BAANBB27-1; ".
SEQUENCE 74 AA, 3338 MW, 7106F48FCDF6158F TEGF4;
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                                          Peptides binding to the DNA binding domain of transcription factor E2F and inhibiting cell cycle progression, useful for the treatment of
                                                                                                                                                                                                     WPI; 2000-532806/48
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                                                                           disorders such as psoriasis and restenosis.
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                     315-1 Wat 1 Wa
                                                                                                                                                                                                                                                                                                                                                                                                      the DWA binding bowin of transcription fac-
dydio progression, useful for the treatment
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RESULT 5
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                                                                                                                                                                                                                                               Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                  receptor receptor can serve as a tool for the drug design of novel therapeutic agents for various indications, including cancer, tumour reduction or prevention), platelet aggregation (as an anti-coagulant), vascular restenosis, arthritis (as an anti-inflammatory), wound healing, tissue regeneration (preferably skin and nerve regeneration) blood coagulation, osteroprorsis (hone regeneration), and cosmetic uses (preferably the prevention of abnormal growths or scarring or for augmentation). This receptor can additionally serve as a tool for the drug design of novel therapeutic agents for indications including ischaemic heart diseases (e.g. myocardial infarction and angina performs). Stroke due to representations of the provential infarction and angina including the receptor can additionally serve as a tool for the drug design of novel therapeutic agents for indication and angina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This invention describes a novel nucleic acid (I) encoding a human lysophosphate acid (LPA; 1-acyl-glycerol-3-phosphate) receptor. Probables which hind to the LAP receptor can be used for detecting expression of a mammalian LPA receptor. The probe can be used for expression predignosition to a discrete associated with LPA receptor activity. The transpectic animals incorperating the LPA receptor activity of mammalian LPA receptors, or for identifying an (ant)agonist activity of mammalian LPA receptors, or for identifying an (ant)agonist
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ***HMTHY Toll invanion, neurotransmitter release; chemotaxis, cancer; drug design; tumour; anti coagulant; vascular restenosis, arthritis; anti-inflammatory; wound healing; tissue regeneration; bodo coagulation; nerve regeneration; osteoporosis; bone regeneration; cosmetic; scarring; ischaemic heart disease; myocardial infarction; angina pectoris; stroke; cerebral infarction; cerebral sequelae; subarachnoid haemorrhage; bening prostation hyperplasia; diabetes melling, refinggathy, neuropathy, neuropathy.
                     AAY0549% standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   activity of mammalian LPA receptors, or for identifying an (ant)agonist capable of alleviating a physical or behavioural abnormality associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDR; AAX78130
                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         with activity of LPA receptor. LPA receptors produce a wide range of responses such as cell proliferation, stimulation of neurite retraction, planelet aggregation, smooth muscle contraction, tumour cell invasion, neurotransmitter release, chloride efflux and chemotaxis. The human LPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 9; Fig 3A-B; 121pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lysophosphatidic acid receptor sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10-DEC-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                        infarction and cerebral sequelae after subarachnoid haemorrhage), benign prostatic hyperplasia, complications of diabetes mellitus (e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               nephropathy; diabetic retinopathy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17-JUN-1999
                                                                                                                                                                                                                                                                                                                                                         retinopathy, neuropathy, and nephropathy), and diabetic retinopathy
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                                                                                                                                    VRWHF 102
                                                                                                                                                                                                                                                                                                                 372 AA;
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RESULT 6
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                                                                                                                                                                                                                                                                           LPA receptor, EDG-2; lysophosphatidic acid, phospholipid, tumour; rell signalling, MAP kinase; LPA modulator; neurodegenerative direase; Alrheimer's disease; Parkinson's disease; neuron damage; apoptocis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to methods of detecting (ant)agonist, inverse agonist or allosteric modulators of the lysobosphatible and the egents agonist or allosteric modulators of the lysobosphatible and read to EEG-1, EEG-2, FEG-3, FEG-4, FEG-5, and EEP-24. The methods are used to identify (ant)agonists and allosteric modulator of the lysophosphatidic acid (LPA) EEG2 receptor, e.g. to treat LPA signalling mediated disease acid (LPA) EEG2 receptor, e.g. to treat LPA signalling
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EPG-1, EPG-2, EPG-3; EPG-4, EPG-5, PSP-24, human, detection; therapy; inverse agenist; allosteric modulator, lysophosphatidic acid receptor; LPA signalling mediated disease; cellular apoptosis.
                                                                                       WO200112838 · A2
                                                                                                                                               Mus sp
                                                                                                                                                                                                                                                                                                                                                                                                       LPA receptor-related amino acid sequence #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAUC0227 standard; Protein; 373 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    such cellular apoptosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; Page 58-60; 63pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Identification of (ant)agonists of LPA receptor EDG-2 for, e.g. treating LPA signalling mediated diseases such as cellular apoptosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Erikson J, Goddard JG, Kiefer M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10-OCT-1997;
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                                                                                                                                                                                                                                             ischaemic heart disease; viral; HIV; inflammatory bowel disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This sequence represents human PSP-24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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100.0%; Fi
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                      Toxin abook, blend endetexin removal, serum, diagnostic te
symples release onto 1, treatment, pertuasis, kusterial
NTV related infections; polymyxin P; Group II.
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                     11-FEB-1991;
                                                                                                                                                                                                                                                 Region
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                                                                       10-FEB-1992;
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                                                                                                                                                                                                                                                                                                 Region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              s, Johnstvatice
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                     91US-0658744
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100.0%; Fred. No. 8;
tire o, Mismatches
                                                                                                                                                                                                                                                                      "repeat region"
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Best Lowel v
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epecified sequences of aminoacid(s) and analogs
momentum provention (s)
               Peptides binding to the DNA binding domain of and inhibiting cell cycle progression, useful
                                                                                                                                                                                                                                                                                                                                                 03-AUG-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA binding: transcription factor, E2F, E2F-1, cell cycle; DF activation; transcription; ap-prosis, proliferative disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        reptide which hinds to toosenipties factor ESF 1 1996 binding demain
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                                                                                               WP1; 2000-532806/48
                                                                                                                                               Mueller R,
                                                                                                                                                                                                                                                                                                                                                                                                      WO200044771-A1.
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y 150 mk; Bred. No.
'Nu 0; Mishatches
                                                                                                                                            Montigiani
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5. /.&e+05;
                     for the treatment of
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                                          Query Match
Best Local :
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Best Local s
                                                                                                                            Poptides which bind to the DNA binding domain of transcription factor E2F and inhibit cell cycle progression may be useful as research agents to investigate the interaction between E2F and DP 1, or the activation of transcription by E2F 1/EP-1 heterodimers. They may also be used for inducing apoptosis and/or cell cycle arrost in a cell, particularly for treatment of cancer or other proliferative discretization.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Peptides which bind to the DNA binding domain of transcription factor E2F and inhibit cell cycle progression may be useful as research agents to investigate the interaction between E2F and DP-1, or the activation of transcription by E2F-1/DP-1 betweenters: They may also be used for inducing apoptosis and/or cell cycle arrest in a cell, particularly for treatment of cancer or other proliferative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DMA binding, transcription factor, ECF, ECF 1, cell cycle, DF activation; transcription; apoptosis; proliferative disorder; psoriasis; restenosis.
                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB01508 standard; peptide; 6 AA
                                                                                                                    disorders
                                                                                                                                                                                                                                                                              Pepridos binding to the DNA binding domain of transcription factor and inhibiting coll cycle progression, useful for the treatment of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200044771 - A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Peptide which binds to transcription factor E2F-1 DNA binding domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OR NOV 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example; Page 26; 42pp; English.
                                                                                                                                                                                                                                     Example: Page 26: 42pp; English
                                                                                                                                                                                                                                                                                                                                                           Mueller R,
                                                                                                                                                                                                                                                                                                                                                                                         (PROL-) PROLIFIX LTD
                                                                                                                                                                                                                                                                                                                                                                                                                       26-JAN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    26 JAN 2000; 2000WO GP00227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    disorders such as psoriasis and restenusis.
                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 RWHF 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 RWHF 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                  such as psoriasis and restenosis
                                                                                      6 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                           Kontermann RE,
                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first onery)
                                                                                                                                                                                                                                                                                                                                                                                                                      9958-0001710
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          66.7%; Soore 4; DR 21; 100 0%; pred Mn 7 85.00
                                        66.7%; Score 4; DB 21; L
100 0%; Pred No 7 8e+05;
                                                                                                                                                                                                                                                                                                                                                          Montigiani
                          0;
                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indols
                                                        Length 6;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DF:1,
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                          Gaps
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AAR86145 ID AAR8 XX

AAR86145 standard; peptide; 10

RESULT

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RESULT 10
AAR86140
ID AAF86
  В
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                                            Ş
                                                                                                                                                                                                                                                                 Poptides AARAGO24-R96236 are examples of peptides and their mimerics of this bind to endothelial leukocyte adhesion molecule (ELAM) This complete molecule is a member of the selectin family of receptors and is involved in binding of leukocytes to the vascular endothelial wall prior to complete the peptides bind pref to E-selectin bind by or complete to the peptides bind by the leukocyte, e.g. to a site of inflammation.

Complete the peptides bind pref to E-selectin bind by also bind by the peptides bind by the selectin, and can be used to treat conditions mediated by E-selectin, complete the strong affinity for the selectin receptors and inhibit the binding of the staly lewis (SLo x) compared by the supproteins to be selectin. The peptide are complicated by the selectin binding of the staly lewis (SLo x) inhapes replaced by the selectin be selectin. The peptide of signist binding of HL60 cells to ELAM 1, have one or more peptide of this period by the selectin because one or more peptide.

Complete the selectin because the selection of the peptide of the selectin because the selectin because allower allyled and the selectin because the selectin be
                                                                                                    Query Match
Best Local S
Matches 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Reptide mimetic, endothelial leakhoyte adhecian molecule, ELAM, selectan, recoptor, leakhoyte, vascular wall, endothelium, extravasation; inflammation; sialyl Lewis; cell surface glycoprotein; HL60 cell.
                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 17; 85pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11-MAY-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO9531210-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Anti-ELAM-1 binding peptide #117.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAR86140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAR86140 standard, peptide, 10 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New pepride(s) that bind to endothelial leukocyte adhesion molecule
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI, 1996-010687/01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26-JUN-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (AFFY-) AFFYMAX TECHNOLOGIES NV.
                                                                                               Local Similarity 100.0%, i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 WVRW 4
6 WVRW 9
                                            1 WVRW 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      useful for treating inflammation and other E-selectin mediated
                                                                                                                                                                                                            Ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cwirla SE, Dower Ruhland-fritsch B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                            Α,
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                                                                                                                                                       55.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Dower WJ,
                                                                                                       Score 4; DB 17;
Pred. No. 9.6;
O, Mismatcher
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                                                                                                                                                       Length 10;
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AAR86146
ID AAR
XX
AC AAR
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AC AAR
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ZT 26-
                                                                                                                                                                                                               RESULT 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
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Modified site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New peptide (c) that kind to endathelial leakabyte adheaton molecule \Gamma_{i} - useful for treating inflammation and other E-selectin mediated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Barrett RW, Cwirla SE, Dow
Martens CL, Ruhland-fritsch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Degride mimetin, endothelial leakonyte adherion malerale, FLAM, relection, receptor; leakonyte, vascular wall, endothelium, extravasation, inflammation, binly lewis, cell surface glycopactein, Hidd cell.
                               26-JUN-1996
                                                                                       AAR86146;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Diviliante, Saje II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 discases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI, 1996 CICEPTICI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11-MAY-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23 NOV-1995.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           $00000000 ac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Anti-ELAM-1 binding peptide #117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26 3377-1336
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                                                                                                                                             AAR86146 standard; peptide;
                                                                                                                                                                                                                                                                                                       6 WVRW 9
                                                                                                                                                                                                                                                                                                                                                            1 WVRW 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                           Concervative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        94US-0241054.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       95WO-US06315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TECHNOLOGIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lowerion/gualifiers
10
/note= "contain ami
                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 4; DB 17; 100.0%; Pred. No. 9.6; Mismarches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               eigh, English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "contain amidated C-terminus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Dower WJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Koller KJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 10;
                                                                                                                                                                                                                                                                                                                                                                                                                        ingels
                                                                                                                                                                                                                                                                                                                                                                                         AAWs:
   FXSXWWXDEXCX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Legidder AMSSETTA FATTA for axamples if populder and their minerius contact bind to enduched all lowbryte adhesis in secure (DLAM) it. This contact is a member of the velocite family if receptors and is involved in binding of lesbeytes in the velocite family if receptors and is involved in binding of lesbeytes in the velocite and is inflammation.

On the population if the lesbeytes in the value of inflammation or the population had been a site of inflammation.

On the population and can be used to test with the solventing affinity for the population respective and fall the following inflammation in the population of the first of the first of the first for the population of the first of the first of the population of the population of the first of the first of the population of the first 
                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Openy Match
Best Linal Himilarity
Matches 4, Oliver
                                                                                                          Endothelial leukocyte adhesion
selectin; diagnosis; mimetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Martens CL, Ruhland-fritsch B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WC053110-A1
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receptur, leakaryte, vascular wall, endothelium, extravacation;
inflammation; staly! [ewis; sell curface glycoprotein, HL60 cell.
                                                        Synthetic
                                                                                                                                                                                                         ELAM-1 peptide mimetic #118
                                                                                                                                                                                                                                                                                                                                AAW63963;
                                                                                                                                                                                                                                                                                                                                                                                         AAW63963 standard; peptide; 10 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure, Page 17, 85pp, English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WP1; 1996-010687/01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11-MAY-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11-MAT-1 00%
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                                                                                                                                                                                                                                                                    02 · OCT - 1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (AFFY) AFFYMAX TECHNOLOGIES MV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6 WVRW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 WVEW 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ۵
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cwirla SE,
                                                                                                                                                                                                                                                                    (first entry)
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   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Dower WJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 4) DB 1
1, fred W. 0.6
7, Wismatcher
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Koller KJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 17;
                                                                                                                                             1, ELAM-1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 10,
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AAW63964
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                                                                                                                                                                                                                                                                              RESULT 14
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                                                                                                                                                                                                                                                                                                                                                                           Query Match
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06-MAY-1992;
05-MAY-1993;
11-MAY-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                  E-selectin, e.g. inflammatory conditions. They can also be used for diagnostic purposes, e.g. for identifying the vascular site of E-selectin in vivo or can be coupled to anti-inflammatory or other drugs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                AAM63846-W64054 are peptides and peptide mimetics that bind selectins including endothelial leukocyte adhesion molecule 1 (ELAM-1) and can be used for blocking adhesion of leukocytes to the selectins. The peptides have applications for the treatment of conditions mediated by
                                                                                                                                                                                                                                                        AAW63964 standard; peptide; 10
                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Modified-site
(AFFY-) AFFYMAX TECHNOLOGIES
                                        12-MAY-1995;
                                                                         12-MAY-1995;
                                                                                              17-MAR-1998
                                                                                                                  US5728802-A
                                                                                                                                                         selectin; diagnosis; mimetic
                                                                                                                                                                  Endorhelial levkocyte adhesion molecule 1; ELAM-1, inflammation;
                                                                                                                                                                                         ELAM-1 peptide mimetic #119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 2; Column 93-94; 84pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Peptide(s) or their mimeric(s) that bind to E-selectin - useful for,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1998 249882/22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12-MAY-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17-MAR - 1998
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                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                 1 WVRW 4
                                                                                                                                                                                                                                                                                                              6 WVRW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      treating conditions mediated by E-selectin
                                                                                                                                                                                                                                                                                                               9
                                                                                                                                                                                                                                                                                                                                                                                                 10 AA;
                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ruhland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cwirla SE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               95US-0439817.
92US-0881395.
93US-0057295.
94US-0241064
                             95US-0439817.
92US-0881395.
93US-0057295.
                                                                       92US-0439817
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0; Mismatches
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Pred No.
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RESULT 15
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                                                              Peptide(s) or their mimetic(s) that bind to E-selectin e g rrearing conditions mediated by E-selectin such as condition(s)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   E-selectin, e.g. inflammatory conditions. They can also be used for diagnostic purposes, e.g. for identifying the vascular site of E-selectin in vivo or can be coupled to anti-inflammatory or other drugs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAM63046-W64054 are peptides and peptide mimetics that bind selections including endothelial leukocyte adhesion molecule I (BLAM-1) and can jused for blocking adhesion of leukocytes to the selections. The peptid have applications for the treatment of conditions mediated by
                                                                                                                                                                                               06-MAY-1992;
05-MAY-1993;
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Martens CL,
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Martens CL,
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                                                                                                                                                                                                                                                                                                                                Endothelial leukocyte adhesion molecule 1;
selectin; diagnosis; mimetic.
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                                                                                                          WPI; 1998-249882/22
                                                                                                                                                                 (AFFY-) AFFYMAX TECHNOLOGIES NV.
                                                                                                                                                                                                                      12-MAY-1995;
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93US-0057295.
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100.0%, Fr
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                                                                                                                                                                                                                                                                                                                                           ELAM-1; inflammation;
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                                                                                    useful for,
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AAW63846-W64054 are peptides and peptide mimetics that bind selecting including endothelial leukocyte adhesion molecule 1 (ELAM-1) and can used for blocking adhesion of leukocytes to the selectins. The peptid

Example 2; Column

91.92,

84pp; English.

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Maximum DB seq length: 200000000
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Pending Patents AA Now:*

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2: /cgm2_6/prodara/1/paa/Ts06_NEW COMB pep:*

3: /cgm2_6/prodara/1/paa/Ts06_NEW COMB pep.*

4: /cgm2_6/prodara/1/paa/Ts08_NEW COMB pep.*

5: /cgm2_6/prodara/1/paa/Ts06_NEW COMB pep.*

6: /cgm2_6/prodara/1/paa/Ts06_NEW COMB pep.*

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30 539 Million cell updares/sec
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Pred No is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total store distribution

SUMMARIES

Result		* Query				
No.	Score	Match	Length	DB	ID	Description
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2	4	66.7	٠, د.	_	T 11500-34001 37	guence
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APPLICANT: DGI BioTechnologies, Inc.
FILE REFERENCE: 2598-400900
FULL REFERENCE: 2598-400900
CURRENT MAPPLICATION NUMBER: POT/HEO/34021
CURRENT BILLING DATE: 2002-10-24
PRIOR ACPLICATION NUMBER: C0/34, IO:
PRIOR FILING DATE: 2011-10-24
NOTHER OF SEQ ID MCS: 537
SCOTMARKE: PAtentin version 3.1
SCOTIMARE: Patentin version 3.1
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/ OTHER INFURMATION: VEGERI-20F
PCT-US02-34021-373
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/ Sequence 422, Application Ed/TES0234001
/ GENERAL INFORMATION:
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Best Local Similarity 100 0%; Pred No. 88;
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OTHER INFORMATION, VEGIRE-20F-Alle
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OF SEQ ID NOS: 15438
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APPLICANT MADD, APPLICATION

APPLICANT DESCRIPTION

APPLICANT DESCRIPT, VASIT

APPLICANT DESCRIPT, LAVID

APPLICANT MAISTRUCKS, ASAU

APPLICANT MAISTRUCKS, JOAN FLANCILS

APPLICANT MADD, JOHNS
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LENGTH: 52
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APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: Compositions and Mathods for the Therapy and Diagnosis of Acnes FILE REFERENCE: 210121.51401
CURRENT APPLICATION NUMBER: PCT/US02/32727
CURRENT FILING DATE: 2002-10-11
NUMBER: OF SEQ ID NOS: 30992
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APPLICANT: Jailet
APPLICANT: Baith, Brenda
MITHITMIT Flugiuss, John
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Rg No NO 13934
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CROMISM: Homo capiens
ERATURE:
CHEEF INFORMATION MAP TO ACC12143.1
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GRGANISM: Propioni acnes
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Cen, Shyian
Bodes, Michael
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Wang, Siging
Jen, Shyian
Lodes, Michael
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Jones, Robert
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Benson, Darin
Jones, Robert
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Sequence 5526, Application US/10087498

Sequence 5526, Application US/10087498

GENERAL INFORMATION:

APPLICANT: Mitcham, Jennifer
APPLICANT: Secity Vasir

APPLICANT: Persing, David

TITUE OF INVENTION Compasitions and Municide for the Theory and Diagnosis of Atness to FILE REFERENCE, 200121,514

FULL REFERENCE, 200121,514

CUMPENT APPLICATION NUMBER - US/10/057,499

CUMPENT APPLICATION NUMBER - US/10/057,499

CUMPENT APPLICATION NUMBER - US/10/057,499

CUMPENT SEC IT NOS: 29212

SEC ID NO 5020

LENGTH: 52
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US-09-978-825-5526
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CURPENT FILTH SATE PAGEATION
NUMBER OF SEC ID NOS: 30992
SEC ID NO 5426
LENGTH: 52
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Best Local (
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APPLICANT: Douglass, John TITLE OF INVENTION: Compositions and Markeds for the Therapy and Diagnosis of Acres FILE REFERENCE: 210121.51401 CURRENT APPLICATION NUMBER, PCT/US02/32727 CURRENT FILING DATE: 2002-10-11 NUMBER OF SEQ ID NOS: 30992
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ORGANISM. Propioni acnes
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Benson, Darin
Jones, Pobert
Carter, Darrick
Barth, Brenda
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Barth, Brenda
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Jen, Shyian
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Phatia, Ajay
Maisonneuve, Jean Francois
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ion na, Fred M: 1 hein;
rive n; Mismatches n
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10: 1:9e+02
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                                                 ; LENGTH: 56
; TYPE: PRT
; OFGANICAM: Frepioni acnes
US-10-057-498-7189
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                                                                                                                                                                                                                                                                                                   US-10-057-498-7189
                                                                                                               APPLICANT: Nitcham, Jennifer
APPLICANT: Skeiky, Yasir
APPLICANT: Skeiky, Yasir
APPLICANT: Persing David
TITLE OF INVENTION Compositions and Markeds for the Theory; and Diagnosis of Action
FILE REFERENCE: 210121.514
CURRENT APPLICATION NUMBER: US/10/057,498
CURRENT FILING DATE: 2001 04 20
UNMARE FOR SE2 ID NO. 20010
SEQ ID NO. 7189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Barth, Brenda
APPLICANT: Douglass, John
TITLE OF INVENTION Comp. sit in all Mark do for the Thorapy and Magnesic of New
FILE REFERENCE, 210121.514C1
CUERENT APPLICATION NUMBER, US/07/378,825
CURRENT FILING DATE, 2003-01-29
NUMBER OF SPG IN NOS: 30892
SEQ ID NO 7189
                                                                                                                                                                                                                                                                   Sequence 7189, Application US/10057498 GENERAL INFORMATION:
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Query Match
Best Local Similarity
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APPLICANT.
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09-978-825-7189
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Jen, Shyian
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Jones, Robert
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Barth, Brenda
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Bhatia, Ajay
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vative 0; Mismato
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190.0%;
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Score 4;
Fred No.
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Jusen, Brenda

Licant: Douglass, John

FILE REFERENCE: 210121.514C1

CURRENT APPLICATION NUMBER: PCT/US02/32727

CURRENT FILING DATE: 2002-10-11

SEC ID NO 11628

LENGTH: 58

TYPE: DOT
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Matches
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Sequence 31626, Application US/09978825
GENERAL INFORMATION:
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APPLICANT: Wheth, Javid
APPLICANT: Persing, David
APPLICANT: Bhatia, Ajay
TYPE: PRT 
CRGANISM: Propioni acnes 
09-978-825-11626
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                                                                      APPLICANT: Douglass, John TITLE OF INVENTION CONTROL 1100 And Mithelf for the FILE REFERENCE: 210121.51401 CURRENT APPLICATION NUMBER: US/09/978,825 CURRENT FILING DATE: 2004-01-29 NUMBER: 05-070 IP NCC 30900
                                                                                                                                                                                                                                                                                                                                             APPLICANT: Mitcham, Jennifer APPLICANT: Skeiky, Yasir
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US02:32727 11626
                                          ENGTH: 58
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Persing, tax.
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Pharia, Ajay
Maibelneuve, Jean Francois
Thang, Yamni
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I des Michael
Benson, Darin
Jones, Robett
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Barth, Brenda
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Bhatia, Ajay
Maisonneuve, Jean Francois
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Carter, Darrick
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100.0%; Fred. No. 2e-0;
tive 0; Mismatches
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; Sequence 24772, Application FC/TUS0232727
; SEQUENCE 24772, Application FC/TUS0232727
; SEQUENCE INFORMATION:
APPLICANT: Skeiky, Yasir
APPLICANT: Skeiky, Pavid
APPLICANT: Bhatia, Ajay
APPLICANT: Maisonneuve, Jean Francois
APPLICANT: Maisonneuve, Jean Francois
APPLICANT: Chang, Yanni
APPLICANT: Chang, Siging
APPLICANT: Gang, Siging
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US 10-057-498-11626
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GENERAL INFORMATION:
APPLICANT: Mitcham, Jennifer
APPLICANT: Okelky, Yasir
APPLICANT: Checky, Yasir
APPLICANT: Festing, David
TITLE OF INTENTION OF Footbline and Math.de for the Therapy and Diagnosis of Score
Tite Reference, Diolil.514
OURSETH APPLICATION TO WARRE "GA/17/07,498
CURRENT FILING DATE, 2001-04-20
RUMBER OF REQ ID NOS, 27212
                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 30992
SEQ ID NO 24772
LENGTH: 64
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LENGTH: 58
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                                                                                        Query Match
Best Local :
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APPLICANT: Jones, Robert
APPLICANT: Caite, Davick
APPLICANT: Barth, Brenda
APPLICANT: Bouglass, John
TITLE OF INVENTION, Compositions and Mathods for the Therapy and Diagnosic
File Exercise: 10121,51401
CURSENT AFFLIANTIAN NAMES. 207,72507,32727
CURSENT FILING DATE: 2002.00-11
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Bost Total Similarity
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                                                                     Match 66.7%, 9. Local Similarity 100.01, 1 tocal Similarity 100.01, 1
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RESULT 15
US-09-978-825-24772
US-09-978-825-24772, Application US/09978925
Sequence 24772, Application US/09978925
Sequence 24772, Application US/09978925
Septemal Information:
Applicant: Skeiky, Yasir
Applicant: Matcham, Johnifer
Applicant: Matsonneuve, Jean Francois
Applicant: Matsonneuve, Jean Francois
Applicant: Mang, Siqing
Applicant: Lodes, Michael
Applicant: Jen, Shyian
Applicant: Jones, Robert
Applicant: Jones, Robert
Applicant: Jones, Robert
Applicant: Douglass, John
Applicant: Douglass, John
TITLE OF INVENTION Compositions and Mathematical Theorems of Actions
Applicant: Douglass, John
TITLE OF INVENTION Compositions and Mathematical Theorems of Actions
Fills Reference: 210121-514C1
CURRENT APPLICATION NUMBER: US/09/078,825
CURRENT FILING DATE: 2003-01-29
NUMBER OF SEQ ID NOS: 30992
SEQ ID NO 24772
SEQ ID NO 24772
USCONSM: Propioni acnes
Search completed: February 20, 2003, 11:42:48 Job time : 17.6667 secs
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66.7%; Score 4; DB 5; Length 64;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels
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Database :
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SUMMARIES

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globin		149	66.7	4	19
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ALIGNMENTS

A/Status: preliminary A,Molecule type, DNA A,Residues, 1-370 <STO> A,Gross-references, GB AERCS173, HIT 37139811, FITH AAF4313711, Cyspecies: Pseudomonas aeruginosa Cyspecies: Pseg Cone Maegymone Invitator 19-Out-1900 #turt_change 31-Dec 1990 Cyaccession: G83352 PyStover, C.K., Pham, X.Q., Erwin, A.I., Vic yothi, S.C., William, C., H. W.J., M.C., Hri adman, S., Yuan, Y., Brody, E.D., Coulter, S.N., Folger, K.P., Kas, A., Darbig, K., Lic, Jory, S., Olson, M.V., Lory, S., Olson, M.V., Nature 406, 959-964, 2000 В Ş A/Status: preliminary A,Molecule type: DMA A,Residues: 1-301 <STO> A,Tross-references: 38 A A; Gene: mtlR; PA2337 A, Trass-references 38 AEC146-, 1 A, Experimental source: strain PAO1 A/Title. Complete genome sequence of Escudomonas actuginosa FAG1, an opportunistic pathor A/Peference number: AR2950; MIID:20437337; PMID:10084043 transcription regulator MtIP PA2337 [imported] - Pseudomonas aeruginosa (strain PAO) RESULT 1 A96741 C; Genetics: A; Accession: G83352 Query Match 83.3%; Score 5; DB: Best Local Similarity 100.0%; Pred. No. 17 Matches 5; Conservative 5; Micratches 35 VRWHF 39 2 VRWHF 6 TR AECHARIA, MIT 3794-770, FIRM WAS DB 2; Length 301; : h 0 TOOND: ACALD

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R.Matsumoto, A.; Hong, S.; Ishizuka, H.; Horimouchi, S.; Feppu, T.

dene 146, 47.56, 1994

A.Titlle Firell Typeria of the AfeE protein involved in coordary metabolium

A;Reference number: Z24852; MUID:94341568; PMID:8063104

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B.Hoskins, J.A., Alborn Jr., W., Arreld, Jr., Bluszczak, Lr., Burgett, S., Broskins, J.A., Alborn Jr., W., Defkowitz, E.J., Lu, Jr., Matsushima, G., S., Lebiato, D.J., Lee, L.N., Defkowitz, E.J., Lu, Jr., Matsushima, y. P.; Sun, P., Winkler, M.E.

J. Barteriol. 183, 5709-5717, 2001

ArAuthors. Yang, Yr., Young Bullid., M., Zhan, G., Ziri, J., Pairz, P., ArAuthors. Yang, Yr., Young Bullid., M., Zhan, G., Ziri, J., Pairz, P., ArTitler Genome of the Bacterium Streptoconous phenomeniae Strain R6.

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A, Reference number: AST872, MUID. 21423245, EMID:11544234
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RyHawkins, C.E., Borges, A., Perham, R.N.
Bur, J. Biothem. 191, 337 346, 1990
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A.M.D. The archive translated the scale; ITT for recible 16 as Glu
C.Comment. This process is a marker for the chaptering the Comment.
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Frot. Matl. Acad. Cod. Clon. 93, 8641 6646, 1996
A;Tille: Restricted expression of Kaposi satolma-associated herpesvirus
A;Keference number. JC6153, MUID:96270595, PMID:8692871
A;Accession: JC6155
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h, Residues: 1-52 - KTE>
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Opposios Obseptomogous proumoniae
Object 4 17 17 18 #2840000 (CVISION 11 17) HOXI, change 12-001-2001
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A; Residues: 1 62 < ZHO>
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C.Species: busan bespesvinus 8, *agosi sarroma-associated virus
C.D.L. 20 09, 100 Haequeter_revisit. 00 00, 1000 #16-1 htmgs 10 May 2000
C.Aldessian, 106155
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C;Genetics:
A; Molecule type: DNA
A; Residues: 1 % ~HAW>
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; Karp, P.; Romero, P.; Zhang, S. Stonthnor, D.; Kiryazin, T.; Levy, P.; Chen, Y., Weo, Science 294, 2317-2323, 2001

A;Anthors, Yoo, H.; Tarr, Y.; Riddle, P.; Jing, M.; Krespan, W.; Perry, M.; Gordon Karm, Sterr, B.M.

A;Title: The Genome of the Matrical Control of the
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A;Gene: Arvilla
A;Map position: linear chromosome
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A;Accession: T46887
A;Status: preliminary; translated from GR/EMBL/DDBJ
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R;Borges, A.; Hawkins, C.F.; Packman, I.C.; Perham, R.N.
Eur. J. Biochem 194, 98-102, 1990
A;Title: Cloning and sequence analysis of the grous encoding the dihydrolippamide aceryl
Bacillus stearothermophilus.
                 A;Molecule type: DNA A;Residues: 1-102 <HAY> A;Residues: 1-102 <HAY> A;Residues: 1-102 <HAY> A;Residues: 1-102 <HAY> A;Experimental source: ctrain 0157:H7, substrain RIMD 0509952
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A;Molecule type: DNA
A;Residues: 1-98 <KUR>
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CrSpecies: Agrobacterium tumefacions
CrPate: 11-7an-2002 #sequence_revision 11-Jan 2002 #text change 11 Jan-2002
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C:Species: Escherichia coli
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A;Accession: AG3064
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A;Orosa references EM
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sigma lbNS protein - reovirus type 1 (strain Lang)
N,Alternate mames nonstructural protein
C,Species: reovirus type 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    B
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                                                                                                                                                                                                                                  RESULT 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
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E.Trwin, D.I., Zhang, S.; Wilson, D.B.
Submitted to the EMBL Data Library. April 1999
A.Description: Characteristics of a Thormonicspita fisca family 48 exceptibles E6.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A,Introns. 21/2
C;Superfamily: Caenorhabditis elegans hypothetical protein Y9C2UA.
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                                                                                                                                                                                                                                                                                                                          A, Experimental source, strain YX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A,Reference number: Z22783
A;Accession: T44499
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A, Mar position
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A;Accession: T27486
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C/Species, Caenorhabditis eleg
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                                                                                                                                                                                                                                                                                                                                                                A; Cross-references: EMBL: AF144563; PIDN: AAD19950 1
                                                                                                                                                                                                                                                                                                                                                                                                            A; Residues: 1-106 < IRW>
                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: DNA
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                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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14 WVRW 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             53 RWHF 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          39 RWHF 42
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                                                                         1 WVRW 4
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16.5 m 1937 #sequence_projetic 15 %m 1347 #rext
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                                                                             66.7%; Seed. Au.
100.01, Fred. Au.
100.01, Mismatches
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100 0%; Pr
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                                                                                                                                                                                                      .30.02,
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A;Note: host Homo sapiens (man)
(;Date: 30-Jun 1969 Harqueror_tevision 10-Jun-1988 Huext_charge 16-Jul-1929
(;Acception: B26436

K;Munemitsu, S.M.; Atwater, J.A.; Samuel, C.E.

Riochem, Biophys. Res. Cummun 140, 509-514, 1086

A;Title: Biophys. Res. Cummun 140, 509-514, 1086

A;Title: Biophys. Res. Cummun 140, 509-514, 1086

A;Title: Biophys. Res. Cummun 141, 509-514, 1086

A;Reference number: Apollo; MIID:87049709; PMID:2420568

A;Accession: B26436

A;Accession: B26436

A;Accession: B26436

A;Accession: B26436
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G:Date: 03 Mar [19] #wwq.mi.mirit. 04 Mar [17] #fwrt_liatg: [1 Exp [17]]

C:Accestion. 89482;

R:Mibert M.D., Dermody, T.C., Field:, B.M.

J. Virol. 64, 2976-2989, 1990

A:Tible: Cirultare of the restrict rell attachment protein: a mudel for the A:Reference number: A34829; MUID:90244415; PMID:2335823
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ArResidues: 1-119 km/s
ArCross-references: GB:M147/0; MID:g333744, FIDN.AAA17277.1, FID:g333746
ArNote: the authors translared the codon CAA for residue 5 as Glu
CrGenetics:
                             A;Accession: T04366
A;Status: proliminary; translated from TB/FMRI/TDBU
A;Molecule type: mRNA
A;Residues: 1-122 <KIM>
                                                                                                                                                                                                   CyAccession: T04366

CyAccession: T04366

R/KIM, C.Y.: Jecusy, S.Y.; Choe, M.S.; Cheong, Y.H.; Han, C.D.; Cho, M.J.

submitted to the EMSI Data Library, March 1997

A/Denovirion [foliation poi charatherization of early indusible rice genes by a fungal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Map position: segment S1
C:Superfamily: recvirus sigma 1bNS protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sigma lhNS profein - reovirus type 1 (strain Lang)
N,Alternate names: nonstructural profein
C;Species: reovirus type 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Map position: segment $1
C;Superfamily: re-viria ::
                                                                                                                                                                                                                                                                                                                 probable peroxidase (EC 1 11 1 7), carionic - rice (fragment)
C;Species: Oryza sativa (rice)
C;Date: 23-Apr-1944 #sequence_revision 23-Apr-1999 #text_change 11-Jun-1999
C;Accession: TC4366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: GB:M35363, NID.g333632, FIDN.MAM47243.1; FID:g333654
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: genomic RNA
A; Residues: 1 119 - MIB -
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                                                                                                                                                                             A; Reference number: Z15314
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66.7%; Score 4; DR 2; Ler
Local Similarity 100.0%; Pred. No. 1.4e+02;
Ens. 4; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             50 WVRW 53
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A.; Liu, F.; Wollam, C.; Allinger, M.; Boughty, D.; Scott, C.; Lappas, C.; Markelz, B.; Stionse 204, 2323-2329, 2001
A,Titue, C.; Allinger, M.; Boughty, D.; Scott, C.; Lappas, C.; Markelz, B.; A, Markelz, B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 15
B97400
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C;Reywords: oridoreductase
C;Reywords: oridoreductase
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Jub time : 13 secs
                                                      COMPANY CONTRACTORS PROPERTY DO TOUR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: DNA
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Best Length
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Best First eletarity for 6%, Pred. No. 1.46402;
Matches 4, Conservation 6, Michaelber 8;
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D ARSK_STRCO STANDARD; PRT; 799 AA.

D PAPA1; Q9E.02; Q9F.65;

D 10-CCT-1996 (Rel. 34, Created)

JI 16-CCT-1996 (Rel. 44, Last sequence update)

JI 16-CCT-2001 (Rel. 41, Last sequence update)

JI 16-CCT-2002 (Rel. 42, Last sequence update)

JI 16-CCT-2002 (Rel. 42, Last sentetion update)

JI 20-Line/Chreunine protein Rinase afsK (EC 2.7.1.).

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Thomach M.E., James K.E., Harris T.E., Call M.A., Electr H.,

Harper D., Bateman A., Brown S., Chandra G., Chen C W., Collins M.,

Chonin A., Eracor A., J.Le A., Biddig, C., Blanchy T., Howarth S.,

Houng C. B., Misser T., Larke L., Harphy L., Clive E., C'Nell S.,

Rabbinowitsch E., Rajandream M.A., Rutherford K., Rutter S.,

Eugger K., Saunders E., Sharp S., Squares S., Taylor K.

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FETTING TO 27-243.

Medicalast A., Hang S., Ishizuka H., Marinouchi S., Beppu T.,

Westernston T, A., Hang S., Ishizuka H., Marinouchi S., Beppu T.,
This CWTGG FEST entry is applight to be produced by the odd laboration between the Swiss Institute of Bioinformatics and the SMBD catestation the Entry and Bioinformatics Institute. There are no reservoicions on it the Entry and profit institutions of the catestation of the content of the c
                                                                                                                                                                                                                                 "Complete Jenere requests of the model actinomycate Strepts" year coelicolar A3(2).",

Nature 417.141 (47(202)).

Nature 417.141 (47(202)).

FORCITOR: INCLUSED IN THE KERULATION OF SECONDARY METABOLISM BY HOSEBLATIANING, ON BOTH SEE AND THE, THE AFSE GLOBAL REGULATORY BY THIS INVESTMENT IN THE COURT METABOLISM.

19 THAT INVESTMENT IN THE COURT AND SEE RESIDUES.
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Meda K., Umeyama T., Beppu T., Horinouchi S.,

"The aerial myrellum defective plant type of Straptomytes griseus

resulting from A-factor deficiency is suppressed by a Ser/Thr kinase
of S. coelicolor A3(2).";
                                                                                                   between the Swiss Institute of Bioinformatics the European Bioinformatics Institute. There a use by mon profit institutions as long as a modified and this statement is not removed. Use entities requires a license agreement (See http or send an email to licenseaisb-sib.ch).
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01-007-1996 (Pel. 34, Last sequence update)
30-MAY 2000 (Pel. 34, Last annotation update)
Serine/threonine profein kinase afsk (En. 2 7.1 -)
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SMART; SM00219; TYPEC; 1.
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PhosSite;
                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformation, and the PMRE outeration
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DOMAIN 16
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Bur. J. Biochem. 191337-346 (1990).
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01-MAY-1991 (Rel. 18, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical protein in pdhA 5'region (ORFI)
Bacillus stearothermophilus.
Racteria, Firmicutes; Bacillales; Geobacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BINDING
BINDING
                                                                                                                                                                                                                    InterPro, IPP001454, Hlynase/hydrlase
InterPro, IPR000150, Hypothet cof.
Pfam, PF00702, Hydrolase; 1.
PR005ITE, PS01229, COF_1, FAFTIAL.
PP03TTE, FS01229, COF_2; 1.
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PROSITE, PSC01180; PPCTETH KTHASE ST; 1.
PROSITE, PSC01180; PPCTETH_KTHASE_TOM; 1.
PROSITE, PSC00118, PPCTETH_KTHASE_TOM; 1.
                                                                                                                                                      SEQUENCE
                                                                                                                                                                              Hypothetical protein.
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MEDLINE=30345939, FubMed=2200674,
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InterPro; IFF002200; Swr_thr_pkir
Pfam; PF00069; pkinase; I.
                                                                                                                                                                                                                                                                                                                                                                PIP; $10796; $10796.
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                                                Y Match 66.7%, So Local Similarity 100.0%; I nes 4; Conservative 0;
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2 VRWH 5
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                                                   Score 4, DB 1; Pred. No. 27; n; Mismatches
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Best Local
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P21197;
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15 CUN 2002
Globin I.
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Nibert M.I., Derrody T.S., Fields B.M.;
"Structure of the roew rus rell-attachment proteins a wodel for the domain organization of sigma 1.";
[Utrol. 64:2976 2989(1990)]
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**SECURISE T048793, Filbhod-C430560,

**Minemarts U.S.M., Atwarex J.A., Samuri C.E.,

**Minemarts U.S.M., Atwarex J.A., Samuri C.E.,

**Biosynthes.s of recvirus-specified polypoprides Molecular oDNA

**Biosynthes.s of recvirus-specified polypoprides Molecular oDNA

**Cloring and number life recovery of the state of the filter of the second seco
    Mordacia mordax (Southern hemisphere lamprey)
Enkaryona; Metazoa; Chordata; Craniata; Verts
Petronyzuntifundes; Entremyzontidan; Mordacia
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Boowirus (type 1 / strain Lang).
Viruses, dashi viruses, hooviiidau,
NCBI_laxiu=10884;
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907938;
01-AUG-1988 (Rel. 08, Orested)
01-AUG-1988 (Rel. 09, Laut bequence update)
01-FEB-1996 (Rel. 33, Last annotation updat
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                                        Vertebrata; Hypercartia;
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RESULT 9
SUB2_MORMR
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AC P21179;
DI 01-MAY-1991
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H35F; Forces; 2LHB;
Interpro; IPROGRAT; Globin;
H5am; H56542; globin; 1;
EBon; H56542; globin; 1;
EBon; Cayyor (1916); Teansport;
H5an; Cayyor (1916); Teansport;
SEQUENCE 149 AA; 18448 MW; Cocca
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01-MAR-1989 (Rel. 1
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Highlades I., Vidal Y., Bodewald K., Braunitzer
Highlades I., Vidal Y., Bodewald K., Braunitzer
Highlades I., Vidal Y., Bodewald K., Braunitzer
Highlades I., Vidal Ferminal I., State Components I., Edwin Hopper-Seylet 375:49-56(1991).
I OUBUNIT: Monomer.
                                                                                                                                                                                                                                                                                                                                       SEQUENCE:

METHIER TIPHHIL, FubMod.3566915;

HELIARD TI, ELBOWLER, Allaid M., Modell E., Braunitzer

"Primary structure of the minor haemoglishins from the sea la

(Fottermyzen marinum, Gyell-Louata).";

Biol. Chem. Hopper-Seyler 368:145-154(1987).

1- SUBUNIT: Monomer.
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Petromyzon marinus (Sea lamprey).
Petromyzon foremes; Petromyzontidae; Penrel Tyvida757,
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INTERPROS TERROSOSTI, Globin.
Piam, PF80042; globin; 1.
PROSITE; PS01033; GLOBIN; 1.
Hemo, Swyden transport; Transport
Chychenek 144 AA; 1144 MW; Al
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MEDLINE 91248417,
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Q919[1];
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last sequence update)
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Hombrados I. Vidal V. Fodowald V. Braunitzer G., Heszil F.,
"The primary structure of the homoglobins of a southern hemisphere
Lamprey (Mordacia mordax, Cyclostomara) ",
Biol. Chem. Hoppe-Seyler 372:49-56(1991).
-!- SUBBUNIT: Monomer.
                                                                                                                                                                                                                                                     the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. "Isage by and for commodified as this statement is not removed."
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Qiu Y., Maillett D.H., Khapp J., Olson J.S., Piggs A.F.,
"Lamprey hemoglobin Structural basis of the Bohr effect
J. Biol. Chem. 275:13517-13528(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa;
Petromyzontiformes;
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HSSP: P02208; 21HP
                                                                                       InterPro, IPRO02335, MyUALU
PEAM, PEONO42; globin; 1.
PRINTS; PRO0613, MYCGLOBIN; 1
PROSITE; PS01033; GLOBIN; 1
                                                                                                                                                                         EMBL; AF248645; AAF67186.1; HSSP; P02208; 2LHP
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PROSITE; PS01033; GLOBIN; 1
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REQUENCE - 149 AA, 16439 MW, 16-5-56384856A GEC64;
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                                               16311 MW; 5F5355F482FAF74E 7F764;
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100 0%, Prod Mc 40,
Five o, Mismatches
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01-MAP-1989 (Pel. 10, 1
16-00T-2001 (Pel. 40, 1
Globin III.
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01-MAY-1991 (Rel. 18, Created)
01-MAY-1991 (Pel 18, Last seq
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                                                                                          MEDLINE 87184913; PubMed-3566915; Hombrados I , Bodewald K., Allard M., Neuzil E., Braunitzer G.; "Primary structure of the minot haemoglobins from the scallampacy (Petromyzon marinus, Cyclostomata)."; Biol. Chem. Hopper-Seyler Aph:145-154(1987)
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                     PIP; B2F042; B2F042
HSSF; F02208, 2LHB.
InterPro; IPR000971; Globin.
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Feironyiintiformos; Petronyiintidae, Mirdaoia.
Pfam; PF00042; globin; 1. PROSITE; PS01033; GLOBIN; 1.
                                                                                                                                                                                                        Petromyzontiformes; Petromyzontidae;
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Eukaryota, Metarca, Chordata, Craniata, Vertekrata, Hypercartia;
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TE, PS01033, GLOBIN
Oxygen transport;
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InterPio; iExpuss.;
Pfam; PF30042; globin; 1.
PRCSITE; PSC1033; GLOBIN; 1.
PRCSITE; PSC1033; GLOBIN; Transport;
Heme; Cxygon transport; Transport;
'Aprant' 29 29 T -> /
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                                                                                                                                                                                                                                    E RAY CRIVIALLORARIN (1.0 ANGSTROMS)
MELLINE SILUTITY, Pakwad 4(3)496,
Honzatko R.B., Bundilokoro W.A., Irvo
"Refinement of a mijedulak mudel fur
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Hendrickwow W.A., Love W.E., Earle J.,
"Orygos] objustive analysis of sea lamprey hemoglobin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Petromyzon marinus (Sea lamprey).
Bukary 19, Morarda, Bordara, Yandara, Morbetrata, Bypotration,
Petromyzontifizate, Fetromyzontifiae, Fetromyzont
MCGI_TaxiD 7707,
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P02208;
21-JUL-1986
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Globin V.
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J. Mol. Riol. 184.147-164(1985)
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2LHB; 15-APR-91.
3LHB; 20-JAN-99.
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-i- SUBUNIT, Monomer.
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EiParynta, Metazna, Obordata, Oraniata, Vertebrata; Hyporoartia;
Petropyzoutiformes, Petropyzoutidae; Lampetra.
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RESULT 15 CBP4_YEAST

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Search completed: February 20, 2003, 11:24:56 Job time: 12:3333 secs
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                                                                                                                                                            Query Match
Best Local Similarity
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D1-0CT-1994 (Rel. 30, Created)
O1-0CT-1996 (Rel. 34, Last sequence update)
O1-0CT-1996 (Rel. 34, Last annotation update)
CRP4 profein, mitochondrial precursor.
                                                                                                                                                                                                                   CONFLICT
                                                                                                                                                                                                                                                                  PIR; A53928; A53928.
PIR; A53928; A53928.
SGD, S00001406; CBP4.
Mitochandrion; Transit peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hebling U., Hofmann B., Delius H.;
submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.
Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.
FINCTION: ESSENTIAL FOR THE ASSEMBLY AND/OR STABILITY OF
PRIGHTNOT.-CYTOCHEME C RELUCTASE. IT HAS A DIRECT EFFECT ON THE
PRIGHT OF THE PRIESE FOR FORELY, CORE 4, CORE 5 AND
APOCYTOCHEMENE R; IT MAY EITHER BE INVOLVED IN POST TRANSLATIONAL
MODIFICATION OF THE SUBMITS OR IN THE ASSEMBLY OF THE ENZYME.
SUBCELLULIAR LOWATION MITTOCHONDRIAL ASSOCIATED WITH THE INNER
                                                                                                                                                                                                                                                                                                                                            EMBL;
                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licensewisb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Characterization of CRP4, a new gene essential for the expression of ubiquinol-cytochrome c reductase in Saccharomyces corevisiae."; [0] Riol. Chem. 269:21284 21292(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Saccharomyces cerevisiae (Baker's yeast).
Eukaryota, Fungi, Ascomycota, Saccharomycetina, Saccharomycetes;
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                                                                       29 WVRW 32
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170 AA; 20219 MW, PRAFFGZEADFORSKER CPC64;
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CRP4 PROTEIN.
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Maximum DB seq length: 2000000000
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sp_invertebrate:*
sp_mammal:*
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sp_bacteria:*
sp_fungi:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by inalysis of the total score distribution

SUMMAPIES

Result No	STOPE	Query	Query March Length DB	T P	I n	Description
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7	5	83.3	407	1 0	ORPXQ4	_9xxq4
80	4.	66.7	52	16	Q97T74	Q97t74
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ALIGNMENTS

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TOT-MAR-2001 (TEMPLED. 16, Created)

TOT-MAR-2001 (TEMPLED. 17, Last projection upon 101-MAR-2001 (TEMPLED. 17, Last annotation upon 101-MAR-2002 (TEMPLED. 21, Last annotation upon 101-MAR-2002)

Transcriptional regulator MtlR.

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C STRAINFARCO 15692 (PAO);

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X MUDDLING-DOGRESSIT, E.A.M. 1009404);

X SCOVE O.F. File M. 2.T. Erwit A.L. Militylld C.D. Warrence E. A. SCOVE C.F. File M. 2.T. Erwit A.L. Militylld C.D. Walls T. Tilyr W. A. Brody R.L. O''''' T. T. Tilyr E. W. T. F. Walls T. T. Tilyr W. A. Garrher M. T. File M., Fright F. W. T. F. Walls T. T. Tilyr M. A. Chith F. N. Compter S. N. Fright F. W. T. F. W. T. F. Pallore T. T. A. Relzu J., Caller M.H., Him W. F. E. W. Tilyr J. Caller M.H., Him W. F. E. W. Tilyr J. Caller M.H., Him W. F. E. W. Tilyr J. Caller M.H., Him W. F. E. W. Tilyr J. Caller M.H., Him W. T. F. E. W. Tilyr J. Caller M.H., Him W. T. F. E. W. Tilyr J. Caller M.H., Him W. T. F. E. W. Tilyr J. Caller M.H., Miller C. FACT. M. Compter Senton Parkets of Franches M. T. Similarian B.D. Caller M.H., Biller AFAC/XVIJ ELMILY C. TELESSERIETICHME C. T. SIMILARIUM. BELLONG M. THE AFAC/XVIJ ELMILY C. TELESSERIETICHME.
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Best Local
                                                                      Mandalla, Solleria, Cetal
Bovidae, Caprinae, Capra.
NCBI_TaxID=9925,
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98WAWG (TEEWRIED 20, "Postod")
01-MAR 2002 (TEEWRIED 20, Isat sequence of late)
01-UN 2002 (TEEWRIED 21, Isat sequence of late)
Patating phoromone receptor gVIRI.
gVIRI
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PEAM, PECCIES, HTHAPATA
PRINTS; PROCOSS, HTHAPATAC;
SMART; SXC0342; HTHAPATAC;
PROSITE; PROCOSH, HTHAPATAC;
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  SEQUENCE FROM
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Mandalla, Eutleria, Outarilod
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~inuntia, Pecera;
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Jerdeno A.K.,
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Q36C71 (REBURNALL)

Q9EC71;

C1.MAE COO1 (TrEMELIAL 16, Created)

C1.MAE COO1 (TLEMELIAL 16, List) sequence update)

C1.MAE COO1 (TrEMELIAL 16, List) sequence update)

C1.MAE COO1 (TreMELIAL 16, List) son first in spdat
                                                                                                                                                                                                                                                STRAIN-83(2) / M.45;

Bentley S.D., Chater K.F., Coxdono-Tarraga A.-M., Challis G.L.,

Thomson M.E., James K.D., Harris D.E., Quail M.A., Kieser H.,

Thomson M.E., James K.D., Harris D.E., Quail M.A., Kieser H.,

Falper D., Faleman A., From S., Chardis G., Chen C.M., Collins M.,

Francis C. H., Kieser D., Tither A., Hidalgo G., Hornsby T., Fowarth S.,

Falkhin-Mitch E., Sajndham M.A., Fother Frd K., Rutter S.,

Seeber E., Saunders D., Slarp G., Squares B., Squares G., Toylor K.

Marrich T., Michights D., Slarp G., Squares B., Squares G., Farkhill G.,

Marrich T., Michights B., Slarp G., Squares G., Farkhill G.,
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                                                                                                                Hopwood D.A.; "Timplete Budwing II obey Alexe Budwing II obey Alexe Budwing II obey Alexe Budwing II (2002) | EMBL; AL391515; CAC04221.1;
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Bases of Joyann the state of the foreign operations, Cherthy was a finished by the foreign operations.
InterPro; IPR000873; AMP-bind. shocker, E300455; AME_BINDING, Hypothetical protein. Sequence ass AA; 30/46 MW;
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TE; PS50262; S_PROTEIN_RECEP_F1_2;
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e EMBL/GenBank/DDBJ
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Fred. No. 41;
n, Mismit thes
                                                               MACHINE.
      299338598B1F90B3 CRC64;
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Best Local :
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Ol-JUN-2002 (TremHire) 15, Last sequence up
F14023.22 protein.
F14023.23
                                                                                                                                                                                                                                                                                                                                                                            Liu S., Yu G., Land G., Sakano H., Jhaveri A., Lent C., Toriumi M., Chin C., Chion J., Choi E., Gontaloz A., Howing P., Koo T., Li J., Liu A., Pham P., Voysherg M., Altafi H., Rushler E., Chao Q., Conn L., Couway A. B., Hanson N., Johnson Hopson C., Khan S., Kim C., Lam B., Mquyen M., Palm C., Shinn P., Tambunga G., Davis P., Ecker J., "The sequence of RAC 514024 from Arabidopsis thaliana chromosome 1.", Submitted (NOV 1999) to the EMBL/GenBank/DDBJ darabases
       01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last segmence update)
01-JUN-1998 (TrEMBLrel. 21, Last annotation update)
01-JUN-1998 (TrEMBLrel. 21, Last annotation update)
High-affinity lysophosphatidic acid receptor hamalog.
Homo sapiens (Human).
Eukaryota: Motazoa; Chordara: Cramiata, Vorrobrata, Euroloogtomi;
Mammalia: Purberia, Primatos; Catarrhini, Hominidae, Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Arabidopsis thaliana (Mouse-ear cress).

Bukaryona, Viridiplantan, Grappopphyta, Embryophyta, Tracheoghyta,
Spermarophyta, Majarlichbyta, edictrylodos, Ore oudicors, Posidae;
eurosids II, Brassicales, Brassicalead, Arabidopsis
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01-00T 2000 (TrEMBLrel
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                                                                                                              043898;
 NCBI_TaxID-9606;
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PROSITE: PSSOOR2; WD REPEATS 2; 7.
PROSITE: PSSOOR4; WD REPEATS PECTON; 1
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Local Similarity 100 0%; Prod No. 47;
hes 5; Conservative 0; Mismatches 0; Indels
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E 370 AA;
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100.0%; Pred. No. 48;
Five 0; Mismatches
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Q97T74;
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Q1.JUN.2002 (TrEMBLrel 21, Created) of JUN.2002 (TrEMBLrel 21, Last sequence up of JUN.2002 (TrEMBLrel 21, Last annotation Hypothetical 43 R kDa protein.
                                                                                        01-00T-2001 (TrEMBLre) 18, Created)
01-00T-2001 (TrEMBLre) 18, Last segmence update)
01-DEC-2001 (TrEMBLre) 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                  Submitted (PEB:2000) to the EMEMPL, AV080712; AALB6002.1; -.
Hypothetical protein.
SEQUENCE 407 AA; 43791 MW;
                                                                                                                                                                                                                                                                                                                                                                                               Theologis A.;
"Arabidopsis Full Length cDNA Clones.";
Submitted (FEB-2002) to the EMPL/CenBank/CDDJ databases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Arabidopsis thaliana (Mouse-ear cross).
Eukaryota, Viridiplantae, Otroptophyta, Embryopbyta, Trache phyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots, Rosidao;
eurosids II; Brassicales; Brassicaceae, Arabidonsis.
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InterPro; IPR000276; GPCP_Phodpsn
 Streptococcaceae; Streptococcus MCBI_TaxID=1313;
                            Streptococcus pneumoniae.
Bacteria, Firmicutes, Bacillus/Clostridium group, Lactobacillales,
                                                                        Hypothetical protein SP0077
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Sequence
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100 0%; Pred. No
tive 0; Misma
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100 0%; Fred No.
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Tettelin H., Welcin K.E., Fallson I.T., Elson J.A., Road T.D., Persyson S. Heidelperg H. Nabry H. S. Silver H. Fortuna I.T., Chin M., M. Lay, T.F., Welsin M. J. Fortuna I.T., Chayam L.A., White O., Salzberg S.L., Lewis H.E., Fadure D., Chayam L.A., White O., Salzberg S.L., Lewis H.E., Fadure D., Chayam L.A., White O., Salzberg S.L., Lewis H.E., Fadure D., Chayam L.A., White O., Salzberg S.L., Lewis H.E., Fadure D., M., Charles H.G., Fillips J. J., Inskinson I., Fillips J. Wester J.C., Dougherty B.A., Morrison D.A., Hollingshead J.E., Flacer C.M., Dougherty B.A., Morrison of a virulent isolate of Stimphodoucous
                                                                                          Q986NT PRELIMINARY PRT, 61 AA. Q986NT (TREMBLE) 71, Creared) 01-JUN-2002 (TREMBLE) 71, Last sequence update) 01-JUN-2002 (TREMBLE) 71, Last sequence update) 61-JUN-2002 (TREMBLE) 71, Last simulation update Byrotherical protein TRE2763.
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Science 29: 400 pt. (2001);
ENBL, ALCOVIL, AVECARED, 1, TIGR, SP6077;
         Thermoanaerchacteriales,
                               Thermoanaerobacter tengcongensis.
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STRAIN TUMOS,
METHOD COOPS, D.B.W.E. account,
METHOD COOPS, D.B.W.E. account,
METHOD COOPS, D.B.W.E. account D.;
Zhong W., Wang H., Herndler B., Ganem D.;
"Restricted e-plession of Kapuel Matthewarascuciated Leipnevirus
"The stricted will be account to the stricted.".
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4; Conservative
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Conservative (
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100.0%; Fred. No.
zative 0; Mismato
   Thormoanaerobacteriaceae,
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o. 1.7e+02;
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, Thermoanaerobacter
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            DDDDDQQCCCQQRRRRDQ
FFDDQQCCCQXNrcQRrrQ
FFDDQQCCQX
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Eshiny dia Windifflatie, Chr
Spennor ghyri, Mijn lingh)ta,
Ebrhartiface, Crymeae, Oryda
NCBI TaxID=4530;
Strausberg R.,
Submitted (ZAN 2001) to the
EMBL, ECOCO185, AMHC2185.1;
                                                                                                                                                                                                                                       Q93LX1 PRELIMINARY, FRT, 83 AA.
Q99LX1;
Q1-JUN-2001 (TrEMBLrel. 17, Created)
Q1-JUN-2001 (TrEMBLrel. 17, Last sequence up
Q1-JFC-2001 (TrEMBLrel. 19, Last annotation
B1-JFC-2001 (TrEMBLrel. 19, Last annotation
B1-JFC-2001 (TrEMBLrel. 19, Last annotation
B1-JFC-2001 (TrEMBLrel. 19) (Tragment)
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Saluki T., Maksumete T., Tamamite K.;
"Ciyan saliva nippinhare(SAS) genemi. CNA,
clone-Ph459804.";
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STEATH NEWER / JCM11007;

METHINE 11902816, Fulfwed 11997336;

METHINE 11902816, Fulfwed 11997336;

METHINE 11902816, Fulfwed 11997336;

Then II. Than II. Like II. Wally J. The J. Want H. Dany M. Mai II. Man II. Man II. Wally J. The J. Want H. Mai II. Man II. Want H. Wally J. The J. Want H. Man II. Man II. Man II. The Jacobson II. The Jacobson II. Jacobson II. The Jacobson II. Jacobson II. Man II. Man Jacobson II. Jacobson II. Man Jacobson II. Jacobson II. Jacobson II. Jacobson II. Jacobson II. Jacobson III. Man Jacobson II. Jacobson III. Jacobson II
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094CT2; PRELIMINARY; PRT; 76 AA.
01-DEC-2001 (TrEMBLrel: 19, Last sequence update)
01-DEC-2001 (TrEMBLrel: 19, Last apportation update)
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Macmalia, Euleria, Fidentia, Colonognathi, Munidae, Munimae, Mus
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ta, Till-polls, Pooles, Frances/
EMED, Section by John Br.
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Best [socal]
                                                                                                                                                                                                                                                                                                                                   STRAIN=VC1 / DSM 3638 / ATCC 43587 / JCM 8422; Weiss R.B., Dunn D M., Robb F T., Brown it P.; Weiss R.B., Dunn D M., Robb F T., Brown it P.; "The complete sequence of the Pyrococcus furiosus genome."; Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AE010247; AAL81574.1; ".
Hypotherical protein; Complete proteome.
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01-JTM-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JTM-2002 (TrEMBLrel. 21, Last annotation update)
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Grapevine virus D.
Viruses, sspNA phsit
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01-FER-1997 (TYEMMETE) 07, Last sequence update)
01-DEC-2001 (TYEMMETE) 10, Last annotation updat
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Q96812;
01-FEM-1997 (TrEMBLIFE)
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"Properties of grapovino virus D. a novel purative trichovirus
" Plant Pathol 78-15-25/1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Viruses, ssPNA positive strand viruses, NCPI_TavID-51617;
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Hypothetical protein Atu4133.
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Mond'D W., Setthal J C., Faul P., Mond'S B., Almeida N.F. At., Wooll.,

Chura V.K., Zhor Y., Chen L., Ward G B., Almeida N.F. At., Wooll.,

Chen Y., Ballson I.T., Eisen J A., Farp F D., Fewer D., Sr.,

Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C.,

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Gordon-Kamm B., Liao L., Fim S., Hordrick C., Chan C., V., Colan M.,

Gordon-Kamm B., Liao L., Fim S., Hordrick C., Chan C., V., Colan M.V.,

Mootove M., Tingey S. V., Tomb J.-F., Gordon M.P., Olson M.V.,
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Hypothetical protein, Complete proteome.
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crop improvement; linolenic acid.
Protein identification: signal transduction pathway; metabolic pathway, hybridication assay, genetic mapping, gene expression control, promoter,
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| Query Match 68.0%, Goore 40, DB 2; Length 448; Best Lonal Similarity 83.3%; Pred. Mo. 31; | A;Status: preliminary A;Molecule type: DNA A;Residues: 1-448 <sto> A;Cross references GB:HC_061258, NID 97257977, FITH CAPTRACT!;, CIPGE THOCHO C;Genetics: A;Gene A14930950 A;Map position: 4 C;Superfamily: Smega 3 fatty acid depaturace</sto> | RESULT 2 D95362 hypotherical protein AT4g3n950 (imported) - Arabidopsis thaliana CySpecies, Arabidopsis thaliana (mouse ear oress) CySpecies, Arabidopsis thaliana (mouse ear oress) CyDate: 16 Feb 2001 #sequence_revision 16 Feb 2001 #text_change 17 May-2002 CyAccession: D85362 F. anenymous, The European Union Arabidopsis Geneme Sequencing Contextium, The Cold Spring Mature 402, 769 777, 1999 A.Title Sequence and analysis of otherwiseme 4 of the plant Arabidopsis thaliana. A.Peference European ASSCOI, MUICLOCASA488, EXECUTION D85362 A.A.Accession: D85362 | Query Match 88.9%; score 40; DB 2; Length 443; Best Local Similarity 83.3%; Pred. No. 31; Matches 5; Conservative 0; Miumatches 1; Indeln 0; Gaps 0; Qy 1 MVRWHF 6 | A;Accession: T08136 A;Status. preliminary, translated from GB/EMBL/DDBJ A;Status. preliminary, translated from GB/EMBL/DDBJ A;Residues: 1-443 <hit> A;Residues: 1-443 <hit> A;Cress-references: EMBL/LIGHA, NIF 34ETES, FIER/AVACENTINE, FIER/AVACEN</hit></hit> |
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A;Gene: PA2778
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RESULT
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Davis, P.W.
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A,Recidence, 1477 (REC)

A,Pi and a-Private being, J., Le, J., Kutta, V., Woldhor, A., Rehde, M.E.

Rill, P. Jose P. phys. 200, 256 264, 1395

A,Fitter Ratia ellular decain of resolvinghis receptor "FB: disulfide structure,

A,Reference number: 366384, MULD:96004804, PMID:7574684

A,Recention: 566384
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A;Accession: $49465
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catalase (BC 1:11:1:6) - nematode (Onobscerca volvulus)
O;Species: Onobecerca volvulus
O;Date: (0:-Pek-1995 #seguende_neviole: 10-Mek-1995 #tekt_change 04-Mar-200)
O;Accession: $49465
                                                                                                              A. Clube reteriors. EMPL. Maille, Mill. Mill. Stierle, FIII. CM. Level, Filling O/Superfamily: datalase
() Frysk 15. http://rich...hem. in.l. metall.pritein. Laid.coductase
() Frysk 15. http://rich...hem. Hir. For. Ann #riaring predicted
() F. 338/Binding site. heme inch (Tyr.) (axial ligand) #status predicted
                                                                                                                                                                                                            A.Beridusia 1770. mENA
A.Beriduso. 1 400 kHEND
A.Dela retetefore: EMBLINGLI & HillyComela, Elifichelo ecc.i, ElipySU8625
                                                                                                                                                                                                                                                                                                                                                                                                                                                         R;Henkle-Duehrsen, K.J. Submitted to the EMBL Data Library, October 1994
86.7%; Score 39; DB 2; Length 482
55.7%; Fred. NO. 48;
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brain-derived neurotrophic factor receptor predured, where splice form - legal transfer thanes, neurotrophic receptor trans, structured receptor tyrosize kinds transfer (man)

C.Species. Hamo sapiens (man)

C.Pate: 02-Aug-1996 #sequence revision 02-Aug-1996 #text_change il-Jun 1999

C.Pacession: 173631; 118357; \$66384; \$44129

R.Shelton, D.E.; Sutherland, J.; Gripp, J.; Camerato, T.; Armanini, M.P.; Phillips, H.F.
J. Nourosci. 15, 477 491, 1995

A.Title: Human trks: molecular cloning, tissue distribution, and expression of extrace-li
A.Peference number: 156557; MUID:95123473; PMID:7823156

A.C. so referriors GR. GRACHA, WID JORICIO, EIEM.AAB33110.1; PID:g913720 R;Allen, S.I.; Eawbarn, E.; Eukfurl, S.E.; Wilcork, G.E.; Ashuruft, M.; Guirlioth, Menroscience 60, 925-934, 1994 R;Tilbe Clarify of a non-ostal, the folio of human take and distribution of the Arkeference humber: 136367 MUDICIOSEZIEZ, EXID:7936202 A;Accession: 138357 A)Status: preliminary; translated from GB/EMBL/DDBJ A)Molecule type: mENA A)Booldoon: 1-477 <RESS

AyBooldaco, 1 477 KREDY AyBooldaco, 1 477 KREDY

A;Molecule type: protein
A;Acaduse: 31 37,14 42,43 67,143:135,267133,154 13,142 507,3271335,334
C;Comment. This form of the receptor is missing the procein kinase domain

Comperficient course growth factor receptor, high affility, locative fich alpha 2-divrop of Frywords alternative printing, gly-protein, growth factor paceptor; tandem repeat; it sufficient, signal sequence flotters predicted near receptor, chart aplice form formities page 435/Demain. Exain derived near predicted next receptor, chart aplice form formities applicated next products. Factor of the first alpha 2 gly-printing repeat boundary next products applicated next products. The first alpha 2 gly-printing repeat boundary next products applied to the first alpha 2 gly-printing repeat boundary next products. Products are not been producted next products and the first products applied to the first products and the first products are predicted next products. The first products are predicted next products and the first products are predicted next products. The first products are predicted next products and the first products are predicted next products and products are predicted next products. A,Giudu referendes. SDB.1107999, CMIM.600466 A,Map pysition: 9q22.1-9q22.1 Teachse fith alpha 2-dlycopro \ [...

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brain-derived neurotrophic factor procures: burn.

brain-derived neurotrophic factor procures: burn.

W.Alternate names: receptor tyrosine kinase trkB

W.Contains: protein-tyrosine kinase (EC 2.7.1.112)

C.Species: Homo sapiens (man)

C.Species: Homo sapiens

C.Accession: A56853; 156557

R.Makagawara, A.; Liu, X.G., Ikegaki, M., White, P.S., Yamashiro, P.J.; Mycum, L.M.; Bie

Genomics 25, 538-546, 1995

A;Pitle: Cloning and chromosomal localization of the human TPK-B tyrosine kinase receptod

A;Peference number: A56853; MUID:95309922; PMID:7789988

A;Accession A56853; MUID:95309922; PMID:7789988

A;Accession A56853; MUID:95309922; PMID:7789988

A;Accession A56853; MUID:95309922; PMID:7789988

A;Cross-references GP MID:40, MID Gertila, FIDM:AACSIATI 1, FID 383991

A;Statine: proliminary

A;Peference number: Isfatta, Mid:10.5123473; PMID:7823156

A;Accession: 156557

A;Statine: proliminary, translated from GE/EMEL/CDEI

A;Residues: 1-822 cSHE>

A;Residues: 1-822 cSHE>

A;Cross-references GB colored

A;Residues: 1-822 cSHE>
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F;32-38-36-40,100 176,104 104,219 266,302-345/Disulfide bonds #status experiment
F;60,001001,109,205,241,264,090,320,330,300,410/Hadding situ. caikobydrate (Asm)
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F:67-01/Domain lengths rich alpha 2 glycoprotein repeat homology LEPIs

F:92 115/Domain lengths rich alpha 2 glycoprotein repeat homology claps

F:10-138/Domain lengths rich alpha 2 glycoprotein repeat homology claps

F:116-138/Domain lengths rich alpha 2 glycoprotein repeat homology claps

F:139-150/Domain tengths rich alpha 2 glycoprotein repeat homology #status atypical claps

F:430-452/Domain cytosolic #status predicted cTMNs

F:453-822/Domain cytosolic #status predicted cTMNs

F:536-814/Domain cytosolic #status predicted cTMNs

F:536-814/Domain protein kinase homology cFINs

F:536-814/Domain protein kinase homology cFINs

F:536-814/Domain protein kinase homology cFINs

F:544-552/Pomion protein kinase homology cFINs

F:544-552/Pomion protein kinase homology cFINs

F:544-552/Pomion protein kinase homology cFINs

F:547/Active site: Lys #status predicted

F:772/Active site: Lys #status predicted
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A;Cross references OFE 100804,
A;Map position: 9322 1 9322 1
C;Function:
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C;Superfamily: nerve growth factor receptor, high affinity, leading-rich alpha C;glycept
C;Keyworde: alternative oplicing, ATP, autoph-sphorylation, glyciptotein, growth factor
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Local Similarity 80.0%;
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                                                                                                                        4 WIRWH 8
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                                                                                                                                                                                                                                                                                                     Similarity
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80.0%;

    Mismatches

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Pred. No. 69;
                                                                                                                                                                                                                                                                                                 Score 38;
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1 00;
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RESULT

Churcher, C.; Harris, D.; Gentles, S., Hamlin, M., F ; Skelton, S.; Squares, S.

Holtoyd,

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A.Cross references. EMPL.AB030805, FIDE BAAR3183.1
A.Experimental source: strain PAOI
E.St.over, G.F., Pham, X.Q., Etwin, A.L., Milogothi, G.D., Walleder
adman, S., Yoan, Y., Brady, D.C., Techner, G.M., Solger, K.P., Kas
, Lory, S., Olson, M.V.
Nature 406, 959-964, 2000
A.Title Greglete Jamene of Estellations assugators PAOI,
A.Peference number (AR2950, MTTD 20437737, PMID 10984043
A.Accession (B8357)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          grobable protein TS 11 hamolog pfT (similarity) - human
C.Species. Homo sapiens (man)
C.Pate: 21-Dec-1996 #sequence_revision 06-Tun-1997 #fext_change 20-Jun-
                                                                                                                                                                                A,Gene. PA0616
C;Superfamily: Freudomoras serujinosa bypothorical protoin VP2
                                                                                                                                                                                                                                                               A;Molecule type: DNA
A;Pesidues: 1-185 <STO>
A;Oreserreferences GR.AEC.4490; CA
A;Experimental scurre: strain PAO1
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P.Makayama, Y., Takashima, Y., Ishibara, H., Shinomiya, T., Kagoyama, M.; M. submitted to the EMBL Data Library, August 1999.
A;Description: Genetic relationship between bacterishins and bacteriophagos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypothetical protein VP2 (imported) - Pseudomonas aeruginosa
C,Species. Pseudomonas aeruginosa
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A, Accession: T44538
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A;Accession: G01586
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,Makayama, K
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Cate: 11-Jan 1990 #sequence_revision [] Jan-1990 #fext_change 06-9ct-2000
Abcession. T44528, p83570
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Bost Local Similarity 80.0%;
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Nature 200, 277 514, 1093

ApAnchors: Equres, R., Suiston, T.F., Taylor, F., Whitchoad, S., Barrell, B.G.

ApyTitle: Sediphering the tiploy of Mysterium takeralicule from the complete

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A/Accession: AC0441
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A/Accession: AC044
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                                                                                                                                                                                                                                                                                                                                                                                                        Nature 413, 523-527, 2001
A)Tille: Genome sequence of Versible postis, the caucative agent of player
A)Reference number: Apono1; MUID:21470419, pMID:(1896260
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A;Residues: 1-262 .0T0.
A;Cross-references: GB:AE004765; GB:AE004091; NID:g3949580; PIDN:AAG06831.1;
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Nature 406, 959-964, 2000
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G.Ouponfamily: Mycokamherium tukerpulcais hypothetical protein
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C;Superfamily: Symechodocous nitrate transport protein nrtB
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C; Cate: us-leg-lygg #sequence_. .....
C; Accession. E75295
R; White, O; Eisen, J.A.; Heidelberg, J.F.; Hickey, B.K.; Peterson, J.D.; Dodson, M.; Shen, M.; Vamathovan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, M.; Shen, M.; Venter, J.C.; Fraser, C.M.
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
Science 286, 1571-1577, 1999
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A.Fryon (mental colorer strain CDS (Tupont)
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A;Reference number: AB257/; FMID:11743193
A;Anteresion: AD3238
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P29246 escherichia
O04658 arabidopsis
P10265 lartobacill
P30569 streptomyce
P29422 micrococcus
C92462 saccharomyc
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MRIMEN Anabidopsis K.I. Length CECN (Lones (BAFLs) sequenced
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"Gene structure, activity and localization of a catalase from intrapellular basters in cochecerca volvelus";
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Nyoum L.M., Biegel J.A., Brodeur G.M.;
"Cloning and chromosemal localization of the
kinace receptor gene (MTPP2).";
Genomics 25:538-546(1995).
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HSSP; P42321; 20AE
InterEro, IFF002226, Catalase.
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        MEEELINE-ASCERIBE, FubMed 7936200;
Allen S.J., Dawbarn D., EckEord C
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MEDLINE:05123473; PubMed:7823156;
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                                                                               TISSUE-Hippocampus;
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MEDLINE-90309922; PubMed=7789988;
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                                                                                                                         SEQUENCE FROM N.A. (TRUNCATED FORMS)
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COFACTOR: HEME GROUP,
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Eckford S.D., Wilcock S.E., Asheroft M.,
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Interpto, IPR0003006; Ig_MHC.
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FEBM; PF00040; LRRWIT; ITERWITASE.
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EMBL, S76474; AACS13110; ...
EMBL, S76474; AACS3110; ...
EMBL, XT8708; G1AC3571.; ...
ESSP, P66213; IIRK
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15-UN-2002 (Rel. 4), Last annotation update)

16-UN-2002 (Rel. 4), Last annotation update)

Chemist (Soybean), Chittleh, Embryophyta, Transcriptyta, Chittleh, Embryophyta, Transcriptyta, Chittleh, Santonia, Santonia, Santonia, Santonia, Santonia, Fabaucao, Papillundideae, Phareuleae, Glycine, UCDI_TaxID-3847,

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PHOSPHORIZATION WITH ELC-GAMMA-1 (BY SIMILARITY).

INTERACTION WITH ELC-GAMMA-1 (BY SIMILARITY).

INTERACTION WITH ELC-GAMMA-1 (BY SIMILARITY).

INTERACTION (AUTO-) (FOTENTIAL).

INTERACTION
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Cyclic di-GMP binding protein precursor (Gell
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                                                                                                                                                                                                                                                                                                                                          15-JUN 2002 (Rel. 41, 15-JUN 2002 (Pel 41,
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                                                                                                                                                                                                                                                                                                                                                                              P58933;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Transit peptide.
TRANSIT 1
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Oxidiredictase. Fatty a 13 liceynthesis. oil crplast, Membranc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; L29215; AAA50158.1;
                                                                                                                                                                                                                                                                                                                    subunit)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPP001225; FA_decaturase
                                                                                                                                                                                                                                                                                                                                                                                                                                                          251
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ESTEFIETE TO GALACTOLIPIES, SUBSCLIPIES AND PHOSPHATICYLGIYCEPOL
PACTMAY POLYARSATITATED FROLLY AND BELOGGE FORTS (PROPARLE).
SUBSCELLILAR LOCATION CHIOPOPLARIS, MEMBRANE-BOTTS (PROPARLE).
COMAIN THE HISTIFICE MOX SOMAINS VAY CONTAIN THE ACTIVE SITE
AND/ OF BE INVOLVED IN METAL ION BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY: BELONGS TO THE FATTY ACID DESATURASE FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACTION, IMPORTANT CONSTITUENTS OF PLANT MEMBRANES, IT IS THOUSHE
TO USE PERPEDOXIN AS AN ELECTRON DONOR AND TO ACT ON FATTY ACIDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       THE SECOND FORESTAIN IN THE BIOSHTWYSDIE BROWN ORDS OF THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                         WIMWHF 256
                                                                                                                                                                                                                                                                                                                                                                                             XANAC
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m; FD001691; FA_desaturase; 1
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165
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                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
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66.13%
85.03%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        49641 MW;
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Amma subdividito, Xach mobas jeng,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HISTIDINE BOX-1.
HISTIDINE BOX-2.
HISTIDINE BOX-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 36; DB
Fied, No. 30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OMEGA-6 FATTY ACID DESATURASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CHLOPOPLAST (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4F3DF52D4B1A2009 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                             788 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1. 원건
                                                                                                                                                                                                                                                                                                                           (Cellulose synthese regulatory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 424;
                                       , Tortal P I.D
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Rest Local
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01-FEH-1991 (Pel
01-NOV-1995 (Pel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nest specificities."

Hacure 417.459.463 (2002).

PROCTOM: Binds the cellulese synthace activator, bio-()

Cyclic diguarylic acid (c ii JME) (By similarity).

SCDETHIT, Tightly associated with the cellulese synthase subunit (By similarity).

Subunit (By similarity).

PATHWAY: Bacterial cellulese biosynthesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS PPOT entry is copyright. It is produced through collaboration the Swiss Institute of Bioinformatics and the EMH, correction the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long to its institutions on its content is in no way modified and this statement is not removed. Trage by and for commercial entities requires a licence discount for the trage by and for commercial entities requires a licence discount for the trage by and for commercial entities requires a licence discount for the little of the commercial content and the content of the content 
                                                                            gene encoding an unusual zinc finger protein.";
Nature 344.219-223(1990).

FIRETICAL THIS PROTEIN IS A DOSE-COMMITHE FACTOR IN FACILION-
REFERCY VAR-ESATION, THE INACTIVATION IN SOME SELIS OF A GRUE
TRANSLUCTATES HEXT TO HETER-CHROMATH, IT SOULD PLAY A BOLE IS CHECKESOME COMDENSATION.
                                                                                                                                                                                                                              SECTENCE OF 155-1169 FROM N.A.
MEDLINE-20190836; PubMed 2107402;
Fewler G., Giarre M., Farah C., Jauez J., Spierer A., Spierer P.;
"Dependence of position effect yearlegation in prosophila on draw-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cleard F. Matsarskaia M., Spierer E.; "The modifier of gosition effort variegation Comarists of Stock there are two alternative transcripts and seven scattered zing fingers, each preceded by a tryptophan box.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ebkaryeta; Metazoa, Arthropoda, Mandibulata, Pancrustacea; Herapo
Insecta; Pteryjota, Neoptora, Endoptoryjota; Diptora; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID:7227,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-FER-1991 (Rel. 17, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AEC12000; AAM38360.1; ALT_INIT.
This SWISS FROT entry is copyright.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. MEDITINE 19523788; PubMed-7708496;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Suppressor of variegation protein 3-7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUV3
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                                                                                                                                                                                                                                                                                                                                                                                 Nucleic Acids
                                                                                                                                                                                                                                                                                                                                                                                                       Cleard F.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          743 WLRWYF 748
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                                                        SUBCELLULAR LOCATION, Muclear (Probable)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DROME
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      , each preceded by a tryptoph Acids Res 21.796-802(1995).
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                                                                                                                                                                                                                                                                                                                                                                                 Matsarskaia M.,
ils Res. 23.3904
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1_1
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788
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66.7%; Pred. No. 56;
tive 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                           Spierer P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POTENTIAL:

CYCLIC DI OMP BINDING FROTBIN

(, ORCTALF41') (PROTPOC4)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT; 1169 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           update)
  is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0
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MHL cutstation
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Query Match
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Matches 4
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PIP: SCORET, SOCIET,

ELYBRIC, SEGIONISCRE SCHEMENT;

INTERFO, IEROUGHALL BELL MILLE,

INTERFO, IEROUGHALL BELL MILLE,

FIRMS PEOLOGIA, I.

SMART; SWOO355, END COHE,

PROCEITE, ITTILLE, ZIMT ENDER CHEE

NACH ELNG 135 205 COHE,

ZN FING 238 262 COHE,

ZN FING 344 365 COHE,

ZN FING 406 431 COHE,

ZN FING 526 548 COHE,

ZN FING 548 COHE,

                                                                                                                                                                                                                                                                                              SEQUENCE FROM M.A

STRAINS-AD-1 / East zeel / Alud 4sue/;

MEDLINE 96337999, FubMed 8688037;

Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann K.D., Borch Sutton G.G., Blake J.A., FitzGozald M.M., Clayron P.A., Gorgyno J.P.,

Korlavago A.P., Doughton, Tomb J.F., Tomb J.B., Bolch C.I.,

Omerheaf P., Frirkpapes E.P., Wohnstock F.G., Morrick J.M., Glodek A.,

Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Hanna M.C.,

Stotton N.G., Krilyry G.M., Devises G.F., Salaw R.G.,

Couton N.G., Krilyry G.M., Bank W.A., File F.E., Frilk M.C.,

Couton N.G., Krilyry G.M., Salith H.O., Warker C.F., Frilk W.C.,

Klenk H.-P., Fraser C.N., Salith H.O., Warker C.F., Frilk W.C.,

Klenk H.-P., Fraser Sequence of the methanogenic atchaeco, Methanouscus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15-JUL-1998
15-JUL-1998
16-CCT-2001
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Thic OWISS PROT entry in copyright. It is preduced through a collaboration between the Swiss Institute of Bioinformatics and the EMRG outstation the European Bioinformatics Institute. There are no reconstitution on the
                                                                                                                                                     Tannaschil.";
Science 273:1059-1074(1996)
-1-SIMILARITY: BELONGS TO
A.FULGIDUS AF0621.
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Archara, Erryarchara, Matharaa ili Mediahodalderaa
Mediahodaldododusese, Mediahodalderaan
MCBI_faxID=2190,
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Mul207.
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(Rel. 36, Last sequence up
(Rel. 40, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              80.0%; Score 36; DB arity 80.0%; Pred. No. 82; Michaeline 1, Michaeline
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                                                                                                                                                                                         ACETYLTRANSFERASE
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Query Match
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Bost Local S
Sutulno 4
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Q22949;
15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (kel. 37, Last sequence upda
15-UUL-1999 (Rel. 38, Last senotation up
CLUBLE 37, C191 Flughith anythranif
(EC 2.3,1.115) (GPAT).
                                                                                                                                                                                      Wherene, 10097 2; 7809258.
InterPro; IRP00212; Acyltransferase.
Pfam; PF0155; Acyltransferase; 1.
Phospholipid biosynthesis; Transferase; Acyltransferase;
Transmembrane; Miloshondrion; Transit peptide
MITCHINETIN (FOTENTIAL).
                                                                                                       TRANSMEM SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                       This swiss-stor entry is depyright if it produced through the Forepara Sidinformation and the storage by non-profit institute and the storage by non-profit institutions as long as its content modified and this statement is not removed. Usage by and outlies a literary agreement (one buggless by and outlies a literary agreement (one buggless by and outlies readiles a literary agreement.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          use by our profit institutions as long as its content in in the way modified and this statement is not removed. Trage by and for commercial untilize regulates a ligence agreement (See http://aww.izb-sib.ch/announce.co.co.d.ee.chd.ee.chd.tt.litence(ist oft.ch).
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Rhabditidae, Peloderinae,
NCBI_TaxID-6239;
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Pfam: PF00583; Acety transf: 1.

Pypullution: Pypulluransferase; Acyltransferase; Occ
Pypullution: Protoka, Transferase; Acyltransferase; Occ
Pypulluransferase; Acyltransferase; Ac
                                                                                                                                                                                                                                                                                                                                        EMBL; U64847; AAB04876.1; ...
Wormpop; Boaps 2; CB39258.
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TIGR; MJ1207; -.
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109 WARWYF 114
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIMILARITY, BELONGS TO THE STAT / DAFAT FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (Potential).
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Similarity 66.7%;
4, Cuservative
                             Similarity
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Buit C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D., Sorayno J.D., Surron G.G., Blake J.A., FitzGerald L.M., Clayron P.A., Sorayno J.D., Surron G.G., Blake J.A., FitzGerald L.M., Clayron P.A., Sorayno J.D., Surron G.G., Doughages N.S.M., Houstook F.E., Martista J.M., 210484 A., Sorat J.L., Geoghages N.S.M., Weldman J.F., Fihrmann J.L., Ruyyen D., Sorat J.L., Geoghages N.S.M., Weldman J.F., Fihrmann J.L., Ruyyen D., Sorat J.L., Geoghages N.S.M., Weldman J.F., Sadow P.M., Houst M.A., Faline B.P., Penrodovoky M.J., Complet D., France C.M., Smith B.O., Wosen G.F., Venter J.C., Wooden G.F., Wellandschule, Methanologenius Mariande, M.J., Wellandschule, Methanologenius Mariande, M.J., Wellandschule, Methanologenius Met
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RS12_
                                                                                        CBL_ECOLI STANDARD; PRT; 316 AA Q47083; P76353; O1-NOV-1997 [Rel. 35, Created] 01-NOV-1997 (Pel. 35, Last sequence update) 16-OCT-2001 (Rel. 40, Last apporation update)
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Science 273-1058 1073/1096;
FINTLOW EFFTERW NO IS INVIVENTAL THE TEAMSLATION INITIATION STEP (BY SIMILARITY).
STMILABITY PELCHON TO THE SIEP FAMILY OF FIRSS MALL PROTEINS.
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Archan, Euryarchaecta, Methanomomi, Methanomomales,
Methanomaldocomomomae, Methanomaldocomoms
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16-077-2001 (Rel
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TIGR; MJ1046;
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                                     Transcriptional regulator cbl CBL OR B1987.
Escherichia coli.
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36, Last sequ
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90.0%; Brod. Mo. 23,
Pilvo O; Mismatches
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Mau B., Shao Y.,
"The complete genome sequence of Escherichia coli K-12.",
Science 277:1453-1474(1997).
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MEDILINE-97406617, PubMed 9078503;

Piley M., Follado-Vides I., Glasnor J.D., Pode C.K., Mayhew G.E.,

Gregor C., Davis N.W., Kirkpatrick H.A., Gooden M.A., Fose D.J.,

Mau B., Shao Y.;

MAU B., Shao Y.;
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"A new gene, obl, encoding a member of the LysP family of
transcriptional regulators belongs to Escherichia coli cys regulon.";
                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                           Transcription regulation, DNA-binding, Complete proteome DNA_BIND 19 39 H-T-H MOTIF (POTENTIAL). CONFLICT 143 143 A > R (IN REF. 1).
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Interpro; IPP000947; HysP_subst
Interpro; IPP005119; LysP_subst
Ffar, FF00106, HTH 1; 1
Ffam, PF003466; LysR_substrate; 1.
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HSSP; P45600; 1AL3.
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163 WERWH 167
                                                                              1 WVRWH 5
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AE000290; AAC75049 1;
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                                                                                                                                                                                                                                                                                                                            316 AA;
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80.0%;
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Pred. No. 49;
0; Mismatches
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24507;
30-MAY-2000 (Rel. 39, Greated)
30-MAY-2001 (Rel. 40, Last sequence update)
16-007-2001 (Rel. 40, Last sequence update)
16-007-2001 (Rel. 40, Last annotation update)
16-007-2001 (Rel. 40, Last annotation update)
16-007-2001 (Rel. 40, Last annotation)
16-007-2001 (Rel. 40, Last sequence update)
16-007-2001 (Rel. 40, Last sequence update)
16-007-2001 (Rel. 40, Last sequence update)
16-007-2001 (Rel. 39, Greated)
16-007-2001 (Rel. 40, Last sequence update)
16-007-2001 (Rel. 40,
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Interpro; IPRO30547; HTH LysR.
Interpro; IPRO30547; HYSP_subst.
Pfam; PF00126; HTH_1; 1.
Pfam; PF00126; HTH_1; 1.
PRINTO; TROCCO3, HTHLICK.
PROSITE; PS00044; HTHLICK.
PROSITE; PS00044; HTHLICK.
TROCCO3, HTHLICK.
PROSITE; PS00044; HTHLIVSE PAMILY; 1.
TROCCO3, HTHLICK.
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Grogenes.";
G. Bacteriol 175:2107-2115(1993).
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MEDINE 93209957, FubMed 6458853;
Schwacha A., Bender R.A.;
                                                                                                                                                                                                 NCBI_TavID 155892;
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"A Caulobacte: ENA methyltransferase that functions only in predivisional cell.";
J. Mol. Biol. 235:472-485(1994).
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Mammalia, Butheria, Primates, Catarchini,
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MEDLINE-99156852; PubMed 10036181;
MEDLINE-99156852; PubMed 10036181;
Marchese A., Sawzdargo M., Nguyen T., Cheng R., Heng H.H., Nowak T.,
Im D. S., Lynch K B., George S.B., O'bowd B.F.;
"Discovery of three Gevel orphan Geprotein-coupled receptors.";
"Discovery of three Gevel orphan Geprotein-coupled receptors.";
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PRINTS; FR00237; GFCRHUGDFSN.
PROSITE; PS00237; G_FPOTEIN_RECEP_F1_1; FALSE_NEG.
PROSITE; PS00237; G_FPOTEIN_RECEP_F1_2; 1.
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m SWISS-PPOT} entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STPAIN-CV. STELLAR; Brunel D.; Fourmann M., Broger N., Brunel D.; Fourmann M., Broger N., Brunel D.; Fourmann M., Proger N., Brunel D.; Fourmann M., Broger N., Brunel D.; Fourmann M., Broger N., Brunel G., Franklinder M., Broger S., P., Brunel, AFZ-9491, AARCHESS.1; F., InterPro. IPR001225; FA_docaturass.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Mognollophyta, eudicotyledons, core eudicots, Posiceurosids II; Brassicales, Brassicaceae, Brassica.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Omega 6 reductase (Fragment)
FAD6 BN 1.
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01-JUN-2002 (TrEMBLrel.
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01-,TIN-2001
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Propom; PDOOLORI; FA_desaturase; 2
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(TrEMBLrel. 17, Last sequence update)
(TrEMBLrel. 21, Last annotation update)
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Pred. Wo. 32,
o, Mismatches
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     WEST BANKAND
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32,
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PRESILT 8
PRESILT 9
PRESIDENCE CONTROL OF PARTICULAR PROPERTY PARTICULAR PART
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Bentley S.D. Charer K.F. Cerdeno-Tarraga A.M. Challis G.L.,

Thomson M.P. James K.D., Harris D.E., Quail M.A., Kieser H.,

Thomson M.P. James K.D., Harris D.E., Quail M.A., Kieser H.,

Halper D., Bareman A., Goble A., Hidalyo J., Hornsby T., Howarth S.,

Cronin A., Fraser A., Goble A., Hidalyo J., Glovelt K., O'Neil S.,

Huang C.-H., Kieser T., Larke L., Mulphy L., Glovet K., O'Neil S.,

Pakbingwitsch E., Pajandream M.A., Putherford K., Purter S.,

Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.

Marren T., Nietzottek A., Woodward J., Barrell B.G., Parkhill J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SSGB6Ö
                       SEPANENCE EPOM N A
SEPANENTO 15602 / PAOI;
MEDIINE-20437337, PubMed-10984043;
MEDIINE-20437337, PubMed-10984043;
SHOVEY C F , Pham X -Q T , Erwin A L , Mizognobi S D , Warrener P ,
SHover C F , Pham X -Q T , Erwin A L , Mizognobi S D , Lagrou M ,
Garber R.L , Geltry L , Teleprino E , Mesthrock-Wadman S , Yuan Y ,
Bacdy L L , Ceulter S H , Felger F F , Mesthrock-Wadman S , Lim R M ,
Smith K.A. , Spender D.H , Wood G K C , Wu C , Paulsen I T ,
Smith K.A. , Spender D.H , Wood G K C , Wu C , Paulsen I T ,
Smith K.A. , Spender D.H , Wood G K C , Wu C , Paulsen I T ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q91065;
01-MAR-2001 (TrEMBLYel 16, Croated)
01-MAR-2001 (TrEMBLYel 16, Last sequence update)
01 (TRI 2002 (TrEMBLYel 21, Last apportation update)
Hyperherical protein PA2778.
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01-MAY-2000 (TrEMPLre) 13, Last sequence update)
01 CTR 2002 (TrEMBLre) 21, Last annotation update)
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gcelicolor A3'2) ";
Mature 417'141'147 (2002).
EMBL, A1136509 CAR66176.1, -. ST21246SEFIBIDSC CRC64;
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genome sequence of Pseudomonas aeruginosa PAO1,
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66.7%;
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Fred. Me 72;
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                                                                                                                                                                                                           . Warrener P.,
" "Adrou M.,
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Mammalia, Eirboria,
Bowidae, Caprinae, Capra
NCRI_TaviD=0026;
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THE PROPERTY PROPERTY BASE 739
INCLEDED INDEPONDED 739
INCLEDED 1120001440, TRE
FINA, BROARTON FLANGUAGE 739, 1
HYDOTherical providing Complete proteomes
HYDOTherical providing Complete proteomes
EXTENDE 137 AA, 32016 MM, 36A41006E0F0TUEL MEYON,
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                                                                                                         Atabilitatis thalland (Monservat dress). Emberyota, Visidipilatho, etraphoghyra, Emberyota (Visidipilatho, etraphoghyra, Emberyota (Visidipilatho), audinotylodhos, etrasids (i. Brassicales; Brassicades), Atabi NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                            Q9M9G2 PRELIMINAPY; FPT;
Q9M9G2 (TrEMBLrel 15, Created)
01-0CT-2000 (TrEMBLrel 15, Created)
01-0CT 2011 (TrEMBLrel 15, List sequence)
01-0CT 2012 (TrEMBLrel 21, List annotation)
E14C23 12 piction
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Eukoryono, Menare, Obirdata, Oraniata, Vertekrata, Euteleostomi,
Mammalia, Europoria, Conarticolotyla, Euminantia, Perora, Rovoidea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAR-2002 (TrEMBLIP) 20, Creared)
01-MAR-2002 (TrEMBLIP) 20, (ast segmente grinte)
01-MIN-2002 (TrEMBLIP). Last annotation update)
Putative phenomena twentil gVIF1.
GVIR1.
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Strike
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Regrette 3.4 W.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BUE HMANN FUE
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s, Conservative
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FROM N.A.
V. COLUMBIA;
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                                                                                                                                                      Brassicaceae, Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                          Last sequents update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             North Vi, 28 6, Debyik (*),
prod Mo. 66,
N. Midwatthes (*), Infelo
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                                                                                                                                                                                  Embryophyta, Tracket
adons, orre endicates,
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                                                                                                                                                                                      Trocketphyta;
idiosts; Posidae;
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RESULT
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Best Local Similarity
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Theologis A.;
Theologis A.;
Thabidipsis Exil Length DNA Clused.",
Submithed (PEP 2000) to the EMBL/MonBank/DEPJ diribises
EMBL, Argeoize AALRECODIT, -.
Hypothetical protein.
Reflects 4.77AA, 4270 MM, 71LT7 MICTORGAN CROSH,
Reflects 4.77AA, 4270 MM, 71LT7 MICTORGAN CROSH.
                                                                                                                                                                                                                                                                                                                                                                                          SETTERTH FRIM M.A. Sakano H. Pham P.K. Banh J., Chung M.K., Yasada F., Liu S.X., Sakano H. Dham P.K., Banh J., Chung M.K., Yasada F., Liu S.X., Sakano H. D., Toriumi M., Yu G., Bowser Goldsmith A. D., Chen H., Chenk P., Hayashiraki Y., Ishida T., Jone Kamiya A., Karlin Noumann C., Kawii J., Kim C., Lam P., Lin J., Mirada M., Bandaka W., Egyyen Y., Palm C.T., Sakurai T., Cacc Seki M., Shinn P., Southwick A., Shinneaski K., Davis R.W., Ecke
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Arabidopsis thaliana (Mouse-ear cress).
Eckasysta, Virtdislantae, Stieffe, Bid., Embrytskyta, Tietbogtkyta,
System (Mytyra, Magya Horpyta, evolit tylediss, tyre evolit te, Ecold
euroside II, Brassicales, Brassicanesa, Arabidopsis
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Interpro, IPP001680, WD40.
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>Figuria '77 AA
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SMART; SM00320; WD40; 7.
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   160
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WVRWH
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   164
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                                                                                                                            06. 78,
100.08;
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, Rowser L.,
⊤ , ⊓ones T.,
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Ecker J.
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RESULT 14
Q95K65
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Best Local s
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DIM 2002 (TrEMBLrel. 11, Last annotation update)
Hypothetical 20.3 kDa protein.
Marara fascicularis (Crah earing macagne) (Cynomolgus monkey).
Enkaryota; Merazoa; Chordata; Craniata; Vertebrata; Euteloostomi;
Mammalla: Futheria, Primates, Catarrhini; Cercepithecidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OBWXJ4;
O1-MAP-2002 (TrEMRLFOL 20, Orested)
O1-MAP-2002 (TrEMRLFOL 20, Last sequence update)
O1-MAP-2002 (TrEMRLFOL 21, Last annotation update)
Heart tephic receptor tyrisine kinase type 2 (Fragment)
                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.

TISSUB-MEDULLA OBLONGATA:
TISSUB-MEDULLA OBLONGATA:
TISSUB-MEDULLA OBLONGATA:
TISSUB-MEDULLA OBLONGATA:
Ocada N. Hida M., Firenta T., Tamima P., Iseki K., Hirai M.,
Ocada N., Hida M., Firenta T., Tamima P., Iseki K., Hirai M.,
Suzuki Y., Sugano S., Hashimoto K.;
TISOLATION OF F., Hida M., Tissub-T., Tissub-T.
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EMBL, R4410907; ARL6796R 1; -
InterPro; IRB000372; IRB MForm
Pfam; PF01462; LRRNT; 1.
SMART; SM00013; LRRNT; 1.
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Mammalia; Euthoria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q8WXJ4
                                                                                                                                                                                                                                                  EMBL; AB066522; BAB62201.1; -. InterPro; IPR000372; LRR_Nterm. Pfam; PF01462; LRRNT; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q95K65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Receptor; Kinase.
NON_TER 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TrkB Isoforms, Unusual Gene Length, and Splicing Mechanism.", Biochem Biophys Res Commun 220 (2014 1985 (2001)
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MEDLINE-21656983; PhibMpd-11798182;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID-9606;
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                                                                                                                                                                                               Hypothetical protein.
SECTENTE 178 AA, 20242 MW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cercopithecinae; Macaca.
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4 WIRWH
                                             1 WVRWH 5
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                                                                                                   Conservative
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                                                                                                                   84.4%;
80.0%;
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                                                                                              Score 38; DB
Pred. No. 55;
1; Mismatches
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Pred 11 22;
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                                                                                                                                              DB 6; Length 178;
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RESULT 15

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Search completed: February 20, Job time : 25.3333 secs
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Best Lucal (
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InterPro; IPPONSEN, IG
InterPro; IPPONSEN, IG
InterPro; IPPONSEN, IERMIC.
InterPro; IPPONSEN, LER Cterm.
InterPro; IPPONSEN, LER Cterm.
InterPro; IPPONSEN, LER Merm.
Pfam; PPONSEN, IG; 1
Pfam; PPONSEN, IERCT, 1
Pfam; PPONSEN, IERCT, 1
Pfam; PPONSEN, IERCT, 1
SMART; SMONONS; LERCT, 1
SMART; SMONONS; LERCT, 1
SMART; SMONONS; LERCT, 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QBWXJ6;
01 MAR 2002 (TrEMBIrel 20, Created)
01 MAR 2002 (TrEMBIrel 20, Last segmence update)
01 CHTM-2002 (TrEMBIrel 21, Last and the update)
Memporcaphin receptor tyrusine kinuse type 2 triniated lucturm.
                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE 11656993; PubMed 11798192;
Stollov P., Custren E., Stamm S.;
"Analysis of the Human TrkB Cene Genomic Organization Powerls Nowel
TrkB Isoforms, Unusual Gene Length, and Splicing Mechanism.";
Rinchem Einghya Pess. Commun. (40.1)54-1165(2000).
Binchem Einghya Pess. Commun. (40.1)54-1165(2000).
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Briller, A,J.S., Bacho, M.K.E., Canald, A,A., Tadakg. T.E.A., Caract, M. Alvaroy, F. A.

Briller, A,C.S., Bacho, M.K.E., Canald, A,A., Tadakg. T.E.A., Caract, E.M., Caract, H.

au Mito, E., Couche, C. El Cur, H., Faulhouni, A.F., Friedle, A.C.S.

submitted to GenBank, June 2000

A;Authors Ferreick, V.C.A.; Ferrey, J. E., Friedle, J. E., Friedle, S.C., Franco, M.C., English Canado, M.A., M.E., Kemper, E.L., Kitadima, J.P., Krieger, J.E., Kuxamae, B.E., Laigu Chado, M.A., Maddira, H.M.E., Manino, C.L., Marques, M.V., Martino, E.

A;Authors Martins, E.M.F., Maddira, H.M.F., Manino, C.L., Marques, M.V., Myaki, C.Z.,

F.G., Nunes, L.R., Oliveira, M.A., de Oliveira, M.C., du Oliveira, B.C., Fulminat, C.A.

Rodriques, V., Rosa, A.C. de M., de Eusa Gi., V.E., de Sa, E.G., Santolik, E.V., Sawasak M., Touhay, V., Rosa, A.C.R., da Silva, F.P., da Silva, A.M., Silva dr., W.A., da Silveira, M.,

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AlAuthors, Yoo, H., Tao, Y., Biddle, P., Jung, M., Krespan, W., Ferry, M., Go.
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A; Reference number: AB2577; PMID:11743193
                                     A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58
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E,Wagort Haber, F., Francold, F.A., Fissig, T., Erab, G., Suter, F., Zuber, E., Wagort Haber, F., Stroker, F., Zuber, F., Z
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; Leithauser, B.; Keiler, K.; Cruz, R.; Danson, M.C.; Hough, D.W.;
Jung, K.H.; Alam, M.; Freitas, T.
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CySpecies: Halobacterium sp. NRC-1
CyDate. 00 Feb 2001 #scqwence_revision 02-Feb 7001 #fext_change 00-Feb-2001
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R:Penaudin, J.; Aullo, P.; Vignault, J.C.; Bove, J.M.
Nucleic Acids Res. 18, 1293, 1990
A;Title: Complete nuclearide sequence of the genome of Spiroplasma citri virus SpV1-R8A2
A;Reference number: 509447; WUID:00206799; DMID:2320423
A;Accession: S08449
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Robby F. Filier, J. McCoopenies Robby F. Skownenski, E. Darnes, J. Frebyashi, A. Cirino, submitted to the EMBL Data Library, March 1998

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A;Molecule type: DNA
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R;Lindler, L.E.; Planc, G V; Burland, V; Mayhew, G E; Rlattner, E P
Infect. Immun. 66, 5731-5742, 1998
A;Title: Complete DNA sequence and detailed analysis of the Versinia pestis KIM5 plasmid
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C;Species: spiroplasma virus 1, SpVI
C;Date: 10.-Nun-1991 #sequence_revision 10-Jun-1991 #toxt_charge 07-Doc-1999
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                                                                    A; Molecule type: DNA
A; Residues: 1-78 < REN>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: DNA
A; Residues: 1-76 < HUP>
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A;Reference number: Z18168
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RESULT 12
T42185
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Science 277, 1453-1462, 1997
A.Title: The complete genome sequence of Escherichia coli K-12.
A.Poferonce number: A64720, MUID-07426617; PMID-0778503
                                   C; Accession: T'
P; Burland, V;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman, A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 294, 2323-2328, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hypothetical protein AGR_C_3173 (imported) - Agrobacterium tumefacienn (chruin C)Species: Agrobacterium tumefaciens
C)Spate_ 20-Sep_2001 #sequence_tevision 30 Cep_2001 #text_change 11 Tan 2010
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A;Experimental source: strain K-12, substrain MG1655
                                                                                                                                                                                                                                                                                                                                                                               A; Map position: circular chromosome
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A; Residues: 1-83 < KUR>
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A;Accession: A97568
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;Date: 12 Ser 1997 #sequen
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  Shao, Y ; Perna, N T ; Plunkert, G ; Sofia, H J ; Blattner, F.R
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Nucleic Acids Res. 26, 4196-4204, 1998

AyTitle: The complete DNA sequence of the large mission to plasmid of a AyReference number: Z22068; MUID:98391744; PMID:9722640

AyReference number: Z22068; MUID:98391744; PMID:9722640

AyReference number: Z22068; MUID:98391744; PMID:9722640

AyReference preliminary; trummlated from dp/pMpi/pmpi

AyReference preliminary; trummlated from dp/pMpi/pmpi

AyReference number: PMA

AyReference number: PMPI:ARM74617; PIDM:AXCTIOLES 1

AyReference number: PMPI:ARM74617; PIDM:AXCTIOLES 1

Cycenetis:
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C:Superfamily (mm/nrg)-F.lin T. reji... [mm.n.glib.lin h.m.l.g/
C:Keywords: Reterotetramer; immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ig Kappa chain V region (V kappa 2) - human (fragment)
GrSpecies: Homo sapiens (man)
GrSpecies: 6-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
GrAccession: 837509
R/Klein, U., Kueppers, R., Pajewsky, K.
submitted to the EMBL Data Library, September 1993
A/Description: Human_Ing(+) IgD(+) cells, the major B cell subset in the pur
                                                                                                                                                                                                                                                                                                                                                                                                                                            A, Molecule typo. mRNA
A, Residues: 1-92 <KLE>
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A)ACCESSION: H86783
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A, Note: 17755
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A;Accession: S37509
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()Species: Lactococcus lactis subsp. lactis
()Date: 23.Mar.2001 #sequence_revicion 23.Mar.2001 #toxt_change 03.Aug.2001
()Date: Date: Date: 187701
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50.0%; Pred. No. 2.3e+03;
Live 3; Mismatches v
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This SWISS-Pauf entry is copyright, it is produced through 6 wollaboration between the wiss institute of bilificantials and the EMBE outstation the Embedden Bookinformatics institute. There are no institutionals of the type of prific institutions in this are the first in the way made by one prific institution in this are the first in the way entitled and this statement to be the transcal. Usage by and for commercial entitles requires a liveage aprecent (See http://www.isb-sib.ch/announce/or send an email to licenze the EBLob).
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                                                                                                                                                                                                                                                                                                                                            InterPro, IPR001175; Neur_channel.
Pfam, PF02931, Neur_chan_LBD; 1.
iE.LUTE, IELLUE, IEEE, I.W. CHANNEL;
EUUSECT; Funtsynaptic mumatiumu; Ioniu
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Bukaryota, Motazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Insectivora, Scrividas, Crodiduinae, Crodidu
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virgor: 1195 (Rei. 34, Liest Esquence update)
15 JUN 2002 (Pei. 41, Liest annotation update)
Acetylcholine receptor protein, alpha chain (Fragment).
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                                                                                                                                                                                                                                                                                                                                       Receptor; Postsymaptic
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SUBGELLULAR LOCATION: Three
SIMILARITY, MELONGS TO THE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CUBCNIT: FENTAMER OF TWO ALIHA CHAING, AND ONE EACH OF THE FEITH, AND DAMMA (TO IMMATURE MUSCLE) OF EUGLICH (IN MITTEE
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3; Missatches
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                                                     Copry Match
Best Local Similarity
Matches 3: Conserv
                                                                                                                         CARBOHYD
NON_TER
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"The binding site of the nicetimic acetylcholine receptor in animal species resistant to alpha-bungarctoxin ";
species resistant to alpha-bungarctoxin ";
shochemistry 34:9172-9176(1995).
BIOChemistry 34:9172-9176(1995).
EXTENSIVE CHANGE IN COMPORMATION THAT AFFECTS ALL SUBJUITS AND LEADS TO OPENING OF AN IGN-CONDUCTING CHANNEL ACERGS THE FLASMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Felis silvestris catus (Cat).
Eukaryora, Metazoa; Chordata, Cramiara, Verrekrara, Burelessiomi,
Mammalia; Furheria; Carmiv.ia, Eissipelia, Fulidau, Felis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-00ff-1996 (Pel 34, Last sequence update)
15-UTB-2002 (Rel 41, Last appostation update)
Acetylcholine receptor protein, alpha chain (Fragment)
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P54250;
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                                                                                                                                                                                                                                                                                  EMBL;
                                                                                                                                                                                                                                                                                                                                      the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ui-OCT-1998
                                                                                                                                                                                                                                    InterPro: IPP001175; Neur_channel.
Pfam; PF02931; Neur_chan_LBD; 1.
PP0SITE; PS00236; NEUROTF_ION_CHANNEL; 1.
                                                                                                                                                                                                                                                                                                         entities requires a linense agreement (See http://www.isb-sib.ch/announce/or send an email to licensewisb-sib.ch).
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                                                                                                             SEQUENCE
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                                                                                                                                                                    DISHLED
                                                                                                                                                                                               MON_TER
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63 WKHWVF 68
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                          1 WXXWXF 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUBHINITY PENTAMEN OF TWO ALPHA CHAIRS, AND ONE EACH OF THE RETA CHAIRS, AND CAMMA (IN IMMATCHE MUSCLE) IS ESSIVED (IN MATCHE
                                                                                                                                                                                                                                                                                                                                                                                                                         SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
SUMILARITY RELEATS TO THE LIGHTE PACES FORDS CHARRET FAMILY
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50 0%; Prod No 9 5e+02;
Tidels
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 Mismatches

                                                                 Score 6; DR 1;
Pred No 9 50+00
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ASSOCIATED WITH PECEPTOP ACTIVATION (BY
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Best Local :
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P75147;
16-0CT-2001
16-0CT-2001
                              SEQUENCE FROM N.A.
STRAIN-ATCC 29342 / M129;
MEDLINE=97105885; PubMed-8948633;
Himmelreich R., Hilbert H., Plagens H.,
                                                                                                           Mycoplasma pneumoniae.
Bacteria, Firmicutos, McIlicates, Mycoplasmataceae, Mycoplasma
NCBI_TaxID=2104,
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EcoGene; EG13309; ypjT.
Hypothetical protein; Complete proteome.
SEQUENCE 40 AA; 10070 MW; E101E2E402E8E640 CB064;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is suppright. It is produced through yould be between the Swiss Institute of Painformatics and the EMED Supprish the European Bloinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for common entitues requires a license agreement. See http://www.isb-sbb.bb/acceptor.send an email to license@isb-sib.ch/.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Blattmer F.F., Plunkett G. III, Block C.A., Perna M.T., Burland V.,
Piley M., Collado-Vides J., Glasner J.D., Pode C.M., Mayhew G.F.,
Gregot J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16.007.2001 (Pel. 40, Created)
16.007.2001 (Rel. 40, Last sequence up
16.JUN 2002 (Pel 41, Last annotation
                                                                                                                                                              Hypothetical lipoprotein MFN650 precursor (E09_orf101). MFN650 OF MF192.
                                                                                                                                                                                                                                                                       MYCPN
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STRAIN-K12 / MG1655;
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YPJI OR B2641.1.
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Herrmann R.;
"Complete sequence analysis of the genome of the bacterium Myroplasma
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                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                    61 WRAWNF 66
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CAUTION, THIS IS A CONDECTUAL TRANSLATION. A SPAMESHIST HAD TO BE
CORRECTED IN POSITION OF AND TWO IN FRAME STOP OCCURS HAD TO BE
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(Rel. 40, Last sequence update)
(Pel. 40, Last annotation update)
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50.0%; Pred. No.
Mismat
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Lostr≐ation -
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RESULT 8
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Best Local
Matches
SECURIAN EROW M.A.
TISSUE-Lung,
Strausberg R.;
Cub-cit-ci (Dec.2000)
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"cDNA of
                                                                                                                                                                                   TISSUE BLOOD,
MEDLINE 20440377, P.LM-3 TIS42152,
Zhana Q. H., Ye M., W. X. F., Ren G. X., Zhao M., Zhao C.-J., Eu G.,
Shen Y., Fan H. Y., Lu G., Zhong M., Xu X. E., Han T. G., Chen J. T. W.,
Tao T. Heang Q.-H., Zhong T., Hu G.-X., Gu J., Chen S.-J., Chen Z.,
"Cloning and functional analysis of Towar with Line anally file of the configuration o
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CIQID
SECUENCE
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Mammalia, Eutheria, Primates,
MCB: TaxID-9606,
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Interpro; IPRO1595; Lipoprotein 3.
Piam; PE0038, Lipoprotein 3; 1.
Pronom; E003376; Lipoprotein 3; 1.
PROSITE; PENNOTE; PENEMP_LIPOFFOTEIN;
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HYPOTHETICAL LIPOTECCETH MINGOL
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Catarrhini, Hominidae,
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5 JUL 1978 (Re) 16, Created)

15 JUL 1978 (Re) 16, List sequence of the control of the control
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MELLINE 9030630, FolkMed 7542800;
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Felis Joann F.D., Alome M.E., Miller, J. Clay' o. F.A., Firktos F.
Felis Joann F.D., Alome M.E., Miller, J.A., Goodyne J.D.,
Porte J.D., Shiley F., Did E. T., Glodd A., Edley J.M.,
Meldman J.E., Phillips C.A., Spriggs T., Hedblem E., Cotton M.D.
Ctoular T.E., Banta H.G., Majora T.T., Saddek C.M., Blandon R.
Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoglagen N.S.M.,
Gnohm T.L., McTonald L.A., Shill F.V., Flaret T.V., Shih H.O.,
Veiter J.C.,
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MIM, 603888; -.
Oxidereductaber NAC: Ubuquinone; Mitschendrien; Transit peptide.
Oxidereductaber NAC: Ubuquinone; Mitschendrien (BY 5:HILARITY).
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This SWISS IROT outry is suppright. It is preduced through a fill of between the Swiss Institute of Bioinformatics and the EMBL outre the Fungacian Bioinformatics Institute. There are no restrictions the Fungacian Bioinformatical factors and the content in the Swiss by and profit institution in large as the content in
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EMB1; AF067166; AAR02450.1; ...
EMB1; BC001169; AAR01168.1; ...
Concw, HGRI1.0607; MCDFB1;
MIM. FILLUM, 1997; MCDFB1;
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Q1-JUL-1993 (Rel. 26, Created)
Q1-JUL-1993 (Rel. 26, Last sequence update)
Q1-JUL-1993 (Rel. 26, Last sequence update)
Q15-JUL-1993 (Rel. 26, Last sequence update)
Q2-15-1902 (Rel. 26, Last sequence update)
Q2-1902 (Rel. 26, Created)
Q2-1902 (Rel. 26, Created)
Q2-1902 (Rel. 26, Created)
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Q2-1902 (Rel. 26, Last sequence update)
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Walker J.E., Arizmendi J.M., Dupwis A., Fearnley I.M., Finel M.,

Medd S.M., Pilkingron S.J., Pinswirz M.J., Skebol J.M.,

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bovine heart mitrochondria. Application of a povel strategy for

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TRANSIT 1 36 MITA-HONDRICH
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Mammalia: Entheria: Cenartiodactyla, Puminantia, Ponora, Bovoidea,
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TO BE UBLIQUINONE.

CATALYTIC ACTIVITY: NADH + ubliquinone = NAD(+) + ubliquinol.

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CATALYTIC ACTIVITY: NADH + socoptor NAD(+) + reduced scoptor

CATALYTIC COMPLEX I IS COMPOSED OF ABOUT 40 DIFFERENT SUBUNITS.

SUBCELLULAR LOCATION Mitoschondrial inner membrane; matrix side.
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Actinoptorygii; Neoprorygii; Toloostoi; Ostariophysi; Cyprinidae; Carassius.
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HSSP; P01772; 2FB4.
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Best Local Similarity 500

Matches 57 Or other by
                                                                                                                     INSSE, PROJEZ, IWTL.
InterPro; IEALOUGE, IMMINITERPRO; IPPORTSEE, IMMINITERPRO; IPPORTSEE, IMMINITERPROPERTY IN MART; SMORACE; IGW; I.
Immunoglobalin V region; Si
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20.MAR-1987 (Rel. D4, Created)

21.MCV 1330 (Rel. 16, I331 144-min.m. ipdate)

15.CCI.1990 (Rel. 20, Last amoutation update)

16.FSpps (Main. W-III region CLL preduce (Phormyorid forto))

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Mammalia, Duthoria, primaro, catarchini, Hacillau, H.c.,
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NCBI_TaxID-4932;
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16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Pel. 40, Last annotation update)
Hypothetical protein MPN091 (RO2_orf138).
MPN091 OR MP064.
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Hypothetical protein; Complete proteome.
SEQUENCE 119 AA; 15763 MW; F523865428542709 CEC64;
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Nucleic Acids Res. 24:4420-4449(1996)
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STRAIN-ATCC 29342 / M129;
MEDLINE=97105885; PubMed=8948633;
Himmelreich R., Hilbert H., Plagens H., Pirkl E., Li B.-C.,
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Bacteria; Firmicutes; Mollicutes; Mycopiasmataceae; Mycopiasma.
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10 WSVWTF 15 | Every March Best Local Similarity 50. Matches 3; Conservative | Submitted (MAR-1998) to the Submitted (MAR-1998) to the EMBL; AJCC5012; CAA1C342.1; NON TER 29 28 AA; 3160 MW; | [1] SEQUENCE FROM N.A. TISSUE=BLOOD; Das P , Tiwari G , Garg L C.; "Characterisation of lysozyme | Bubalus bubalis (Domestic warer buffalo). Bukaryota, Metazoa; Chordara; Craniata; V Mammalia; Eutheria; Cetartiodactyla; Rumi Bovidae; Bovinae; Bubalus. NCBI_TaxID=89462; | 2821 1 2821 PRELIMINARY, 062821, 01-AUG-1998 (TrEMBLrel. 01-AUG-1998 (TrEMBLrel. 01-DFC-2001 (TrEMBLrel. 01-DFC-2001 (TrEMBLrel. |
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| PRT; 31 AA.
Created)
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Prod. No. 1.7e+03;
3, Mismatches 0; Indels 0; Capo | EMBL/GenBank/DDBJ databases | .;
me encoding gene promoter in Bubalus | Bibalis hihalis (Domestic water huffalo).
Bukaryota; Metazoa; Chordara; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bubalus.
NCBI_TaxID=89462; | PRT) 28 AA.
Created)
Last sequence update)
Last annotation update) |

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Q1 DEC 2001 (TREMBURE), 19, Cleated)
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Moran P. Rolan Alvarez E.;

Submitted (SEE 2011 *** *** EMRI/GrenFank/FFFZ

EMRI, AF41661; AAL17810 ***

EMRI, AF41661; AAL17812.1; ***

InterFroj IRRO0242*; Cyt.d.ox_2.

Pfam; EF92/93, COX_IM, I.**

Misochondrion
                             Rattus norvegicus (Rat).
Eukaryoti, Motiroi, Obordata, Oxamiata, Vertebrata, Eutoleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi, Munidae, Murinae, Rattuo.
                                                                                                                                      01-NOV-1996 (TrEMBLrel 01, Created)
01 NOV 1996 (TrEMBLrel 01, Last sequence update)
01-MAR 2002 (TrEMBLrel 20, Last annotation updat
Transforming oncogene NEU (Fragment).
NCBI_TaxID=10116,
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Viruses, Resmald Wiruses, Resmald to
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Mesogastropoda; Littorinoidea; Littorinidae; Littorina.
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Cytochrome oxidase subsmit II (Figgreet)
Littorina Last 11:
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S. Michael Bak
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"Teamtification and characterization
neu promoter.";
Mol. (FFT FT)
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Q08615;
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EMPLY Xeedzes CAAA6566.1; -.

MOD, MOI 95410, Errbd.

Transmembrane, Glycoprotein, Doplication, Receptor, Tra

Typicalor protein kinder, ATP bloding, Phosphorylation,

NON TER 49

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                                                                                                                                                                                                                                                          White M.R.-A., Hung M.-C.; "Cloring and Characterization of the mouse new promoter."; "Country and Characterization of the mouse new promoter."; "Characterizactivity all - A FROIBIN IYROSINE - ADP + PTYROSINE PHOSPHATE.
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01:NoV-lyyb (TrEMBErel, 01, List sequence update)
01:NoV-lyyb (TrEMBErel, 12, List sequence update)
01:NoV-lyyb (TrEMBERE) 12, List sequence update)
NoVial ERFIEROREMOTORIO unogene D 2 (EC 2.7.11112) (NEU oncogene)
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Mol. Cell. Biol. 1...000...

EMBG; Moltout; AAAdindo.!; ...

Coccyene, Transforming protein.

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MCET_TAATE 18890;
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Mol. Cell. Biol. 10:6306-6315(1990).
                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM M.A.
MEDLINE 92228498, FulMed=1348855;
                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Merazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                               ERBEZ OR NEU.
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                                                                                                                     CERTRACE
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1. SIMILARITY EQUIVALENT TO HOMAN CERB B-2/HER-2.

LIMILARITY LEDNING TO THE SUF RECEILS FAMILY.
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6 WCRWGF
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                                                          b 100.0%, Score 6, DB Similarity 50.0%, Ered. No. 2.7d 3, Conservative 3, Mismatches
                                                                                                                     49 AA, LOIC MW.
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Rudentia, Guiurognathi, Munidae, Munisae, Mus
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RX MEDLINGE 10365717, PubMed-10916147,

RX MEDLINGE 10365717, PubMed-10916147,

RA Alvar-nam A. 1G. Peinach F.O., Arrida P., Abres F.A., Everying M.

RA Alvar-nam R.D., Alves i. M. C., Araya J. E., Raia G.S., Paprista G.S.,

RA Alvar-nam R.D., Alves i. M. C., Araya J. E., Raia G.S., Paprista G.S.,

RA Alvar-nam R.D., Alves i. M. D., Bordin S., Rove J.M., Parror D.M., Carror H.

RA Follows M.H., Bonacrorsi E.D., Bordin S., Rove J.M., Carror H.

RA Glanton M. B., Calledon A., Cossa M. E.P., Cossa M.P.S.,

RA Hollow M. P., Camargo A.A., Cossa M. C.P., Cossa M.P.S., El Corry H.,

RA Facincami A.P., Epricia A.J.S., Parreira V.O.A., Perro J.A.,

RA Facincami A.P., Epricia A.J.S., Perreira V.O.A., Perro J.A.,

RA Hollow M. P., Camare S.C., Franco M.C., Fromme M. Purlan I.P.,

RA Hollow M. R., Madeira A.M.B., Cossa M.C., Fitajima J.P.,

RA Hollow M. R., Madeira A.M.B., Martins E.M., Lopes S.D., Fitajima J.P.,

RA Marthas E.G. M. Lopes S.A., Lopes S.D., Fitajima J.P.,

RA Marthas E.G. M., Martins E.A., Lopes S.A., Lopes G.P., Marino C.I.,

RA Marthas E.G., Martins E.A., Lopes S.D., Fitajima J.P.,

RA Marthas E.G., Martins E.A., Clivetta M.A., Martins E.A., Miracia E.G., Martins E.M., Notto I.E.S.,

RA Marthas C.F. M., Martins E.A., Clivetta M.A., Janachado J.A.,

RA Menck C.F. M., Martins E.A., Clivetta M.A., Janachado J.A.,

RA Moon D.H., Nagai M.A., Nascimonto A.I. T.O., Notto I.E.S.,

RA Miracia A.C.E., Martins E.A., Clivetta M.A., Janachado J.A.,

RA Menck C.F. M., McDiega F.G., Padrigues V., Je Pesquero J.E.,

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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Primates, Catarrhini, Hominidae,
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A Han C. G., Chisupo E., Mari H., Honda T., Sasakawa L., Jane, A Han C. G., Chisupo E., Mari H., Honda T., Sasakawa L., Jane, A Mihara S., Shiba T., Hartori M., Shibagawa H.;
A Mihara S., Shiba T., Hartori M., Shibagawa H.;
A Mihara S., Shiba T., Hartori M., Shibagawa H.;
PT. C157:H7 and genomic comparison with a laboratory strain V 12.";
PT. DNA Res. 8.11-22(2001).
PP. EMBL, APO124; AAC31491.1; -..
DR EMBL, AP01254, AAG58810.1, ALT_UNIT
EMBL, AP01254, BAB3767.1; -..
FMB., AP012566, BAB3767.1; -..
FMB., AP012566, BAB3767.1; -..
Sp. SEQUENCE EL AA, T286 MW; SP7F44ELLEPD58CD3 CPC64;
Sp. SEQUENCE EL AA, T286 MW; SP7F44ELLEPD58CD3 CPC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D., Pose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A., Posfal G., Hackett J., Klink S., Boutin A., Shao Y., Miller L., Grotbock E.J., Davis M.W., Lim A., Dimalanta E.T., Fotomousis K. Apodara J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C., Welch R.A., Blattner F.R.;
"Genome seguence of enterchaemoxrhagic Escherichia coli O157:47."
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PPOSITE; PS0294; PRENYLATION;
Hyporthetical protein; Complete proteome.
SEQUENCE 50 AA, 7368 MW; EECD70F210030507F CRC64;
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EMBL, AB003865; AAF82939.1; -.
                                                                                                                                                                                                                                                                                                                                                                                MEDIINE-21156231, PubMed-11258796;
Hayashi T., Makino K., Chnishi M., Purokawa K., Ishii K.,
Han C.-G., Chtsubo E., Makayama K., Morata T., Tanaka M.,
Iida T., Takami H., Honda T., Sasakawa C., Cgasawara N., Y
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Molecular evolution of a pathogenicity island from enterthemorphagic escherichia coli 0157:H7.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Perna N.T., Mayhew G.F., Fosfai G., Kaper J.B., Blattner F.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SPECIES=E coli; STRAIN=EDL933;
MEDLINE=99229885; PubMed=9673266;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Escherichia coli, and
Escherichia coli 0157.H7
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Best Local 8
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01-MAR-2001
01-MAR-2001
01-JUN-2002
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HSSP; B00469; HTSV
InterPro: IPR000000; Thymidylat gymt, 1
Pf00300; Ehymidylat gymt, 1
Pr000m; PF0031180; Thymidylat gymt, 1
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Lantebacillaceae, Lactibacilleo.
Noni Takin 1999,
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Submitted (DEC-2001) to the
EMBL, BC017733; AAH17733.1,
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Mammalla, Eutherla, Primates;
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(TrEMBLiel. 16, Last sequence update)
(TLEMBLiel. 21, Last annotation opdate)
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Chaired (TER 1994) to the B
EMBL, UTIE7; AAA6311417
FRITENCE (4 AA, 234) Ma,
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C1 NOV 1996 (TrEMBLrel. 01, Last sequence update)
C1 NOV-1996 (TrEMBLrel. 01, Last sequence update)
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MEDLING-20504483; FubMod=11016950;

Ng W.V., Kennedy S.P., Mahalaas G.G., Berquist B., Fan M.,

Ng W.V., Kennedy S.P., Mahalaas G.G., Thoroson V., Sbrogna J.,

Shakla H.D., Lasky S.R., Ballga W.S., Thoroson V., Sbrogna J.,

Shakla H.D., Lasky S.R., Ballga W.S., Thoroson V., Sbrogna J.,

Shakla H.D., Lasky S.R., Pall C., Dahl T.A., Welti R., Goo Y.A.,

Lutthusser E., Friler F., Frie P., Fanner M.G., Hough D.W.,

Maddocks U.G., Jaklenski F.E., Krebs M.F., Angevino C.M., Dale H.,

Isenbarger T.A., Peck R.F., Pohlschruder M., Spudich J.L., Jung K.-H.,

Isenbarger T.A., Hol S., Faniels C.J., Dennis P.P., Gmer A.D.,

Ebhardt H., Live T.M., Ling T., Fils C.J., Dennis P.P., Gmer A.D.,

Ebhardt H., Live T.M., Ling J., Fils C.J., Dennis P.P., Gmer A.D.,

"Johnson organic S. Hallbarderium species MRC-1.";

Proc. Natl. Acad. Sci. J.J.A. J/:121/6-12181(2000).
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09HST8;
01-MAR-2901
01-MAR-2001
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Actinomycotales; Corymetatterinese; M
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Archaea, Eurgardhaecta, Halobacterium.
Malobacteriaceae, Halobacterium.
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RESULT 13

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RRACOCOS DETECTOR
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BR MBL, AF053947; AAC13243.1; -- DR EMBL, AF074611; AAC82749.1; -- DR EMBL, AF074611; CAB55242.1; -- CEMBL, ALITICIAL (CAB55242.1) -- DR EMBL, AF074611; CAB55242.1; -- DR EMBL, AF074611; AAC82749.1; -- CEMBL, ALITICIAL (CAB55242.1) -- DR EMBL, AF074611; AAC82749.1; -- CEMBL, ALITICIAL (CAB55242.1) -- CEMBL, -- CEMBL, AL
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01-AUG-1908 (TrEMBLrel. 07, Last sequence update)
01-MAR-2-072 (TrEMBLrel. 22, Last annotation update)
Hypotherical protein Vino:
Y1091 OR YEMTL.60C.
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01-MAY-2000 (TREMBLE) 13, Last annotation update)
Hypothetical 9.1 kDa protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lindler L.E., Plano G.V., Burland V., Mayhew G.F., Blattner F.R.; "Complete DNA sequence and devailed analysis of the Yersinia pestis FIMS plasmid encoding murine toxin and capsular antigen."; Infect Immun 66:571-5742(1998)
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Kobayashi A., Brubaker R.R., Gardia E.;
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SEQUENCE FROM N.A.
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Manwaring N.P., Skurray R.A., Firth M.;
"Nucleotide sequence of the F plasmid leading region.";
Plasmid 41:219 225(1999);
Plasmid 41:219 225(1999);
EMBL; AF100229; AAD#7188.1; -.
Hypothetical protein; Plasmid.
                                                                                                                                                                                                                                                                                                                                                                                             Samped G., Misobuchi K.; "Organization and diversification of plasmid jet mos or suplectide sequence of the Pine genome"; Submirted (MAY-1999) to the EMPL/GenPank/DDRJ databases
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(c) 1993 - 2003 - Compagen Etd.
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Pred. Not is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIE

| Result
No. | Score | Query
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Match Length DB | DB | ID | Description |
|---------------|----------|----------------|--------------------------|----------|-----------|--------------------|
| 1 | 6 | 100.0 | 6 | 15 | AAR57386 | Peptide for treati |
| 2 | ת | 100.0 | ·v | 15 | AAR57391 | for |
| نين | 6 | 100.0 | 9 | 21 | AAB01492 | Peptide which bind |
| 4 | 6 | 100.0 | 6 | 21 | AAB01497 | Peptide which bind |
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| ur necrosia f | Consensus Figual p | esuce | ensus si | signa! | د. | ignal | Consensus signal p | gnal | ani | sensus signa | Movel buman diagno | . buman | Hepatitis B virus | Insulin/insulin-li | lin/ | tido which bin | itis GP : | 3 | Actidocal BoEcation | P-dep | 4 | Epitope derived fr | an HLA-DP res | n BLyS bind | phin | egon green 514 | d 11. Eogaf acEoa | for | | Haemophilus influe | Peptide for treati | arion asim | Peptide which bind | D |

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                                                                                           Disclosure; Page 11; 14pp; Japanese
                                                                                                                                                                                                                                               A peptide and an adsorbing agent prepd. by immobilising it on a carrier - useful for treatment of diseases related to anti DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21-MAR-1995
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The sequences given in AAR57386-413 are peptides which are all covered
                                                                                                                                                                                            antibodies and immune complexes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Peptide for treating diseases related to anti DNA antibodies.
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Marther 7, Conservative
Query Match
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A = Trp. Phe or a peptide fragment consisting of 2 residues;
B : Trp. Phe, Asn or Glu;
X and Y - a bond or Asp, Glu, Arg, Lys, His or a peptide fragment consisting of 2-10 residues, provided that at least one
                                                                   X or Y ar Z = OH or NH2; and n = 2-5.
                                                                                                 These peptides may be immobilised on a marrier in the preparation of absorbing agent which may be used in the treatment of diseases realated anti-DWA antibodies and/or immune compex.
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                    Sequence
                                                                                                                                                                                Disclosure; Page 11; 14pp; Japanese
                                                                                                                                                                                                    antibodies and immune complexes
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                                                                                                                                                                                                                                                                                                                                                                                                       Peptide for treating diseases related to anti-DNR antibudies.
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regulded while bind to the DNA binding domain of transcription factor EDF and inhibit cell cycle progression may be useful as research agents to investigate the interaction between EDF and EPF. In the activation for two units by EDF INFO in Providing to They may also be used for inchaining the SEF INFO in Providing to They may also be used for inchaining the six and rest in a cell, particularly for treatment of rancer or other proliferative discreture such as partiasis and restenosis.
Peptide which binds to transcription factor ROF 1 DNA binding domain
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and inhibiting cell cycle progression, useful for the treatment of
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so 0%; Pred Mo. 7.8e+95;
*iv. 3; Mismathbor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 4; Page 9; 42pp; English
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                                                                                                                             Peptide which binds to transcription factor EDF-1 DNA binding domain
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Peptides binding to the DNA binding demain of transcription fact and inhibiting cell cycle progression, useful for the treatment
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                                                              Mueller R,
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                                                                                      (PROL-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
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                                     2000-532806/48
                                                                                                                                                                                                                                                                                                                                                                                                                              WXXWHF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5,
                                                                                     PROLIFIX LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   such as psoriasis and restenosis
                                                              Kontermann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kontermann RE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                               (first entry)
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                                                                                                             993B-0001710
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note: "Any amino acid"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100 0%; Score +; D8 21;
A3 3%; Pred No 7 Re+05;
                                                              RE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Montigiani
                                                             Montigiani
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                              s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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Best Local c
Matchec
                    Query Match 100
Best Local Similarity so o
Matches 2) Consulvative
                                                                                                                                                                       Peptided which bind to the DNA binding 3 "which for incorrigion forms for and inhibit well by the progression may be useful as research agents to investigate the interaction between Bor and Dn 1, or the armivation of transcription by EDF 1/DP 1 between Bor and Dn 1, may also be used for inducing approximation and or total oyste united in a cell particularly for treatment of cancer or other proliferative and contact the second of the second of the proliferative and contact the second of the sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Peptides which bind to the DNA binding domain of transcription factor E2F and inhibit cell cycle progression may be useful as research agents to investigate the interaction between E2F and DF-1, or the activation of transcription by EnF 1/DF 1.644. Simple They may also be used for indicing interaction of capter or other prodiferative a cell, particularly for treatment of capter or other prodiferative as cell, particularly for treatment of capter or other prodiferative
                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                         Republies kinding to the TDM kinding it will for the trial manual and inhibiting the loyele progression, useful for the treatment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WC200044771-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DWA kinding, transcription further FDF; FDF-1; owll activation; transcription; apoptosis; proliferative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AABC1506 standard; poptide;
                                                                                                                                                                                                                                                                                                                               EXample,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26-JAN 1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26-JAN-2000; 2000WO GR00227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      poortagis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Peptide which binds to transcription factor more a communicating for the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     disorders such as psoriasis and restenosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROLIFIX LTD
                                                                                                                                                                                                                                                                                                                          Paye 26; 42pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Paye 26; 42pp; English.
                                                                                                                                                         such as psoriagic and restenosic
                                                                                                               6 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      restenceis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kontermann RE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tarity 50 04,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27, 1000 4566
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                      100.0%; Score 6; DB 21; 50 0%; Prod Mo 7 opins; or victation 7; Victations of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Wishington
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                                                                     Length 6;
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                                                                                                                                                                                                                   ABECCT J
AAET2181
ID AAE
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    Polyglutamine repeat with jon there is disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Poptides which bind to the DNA hinding downin of transcription factor F2F and inhibit cell cycle progression may be useful as research agents to investigate the intention between B2F and DP-1, or the artification in transcription in the B2F and DP-1, may also be used for inducing appropriations cell cycle arrest in a cell, particularly for prestment of compact or other proliferative
                                                                                       Polyglutamine repeat domain binding peptide, QPB1-M7FD.
                                                                                                                                   18-DEC-2001
                                                                                                                                                                                                                      AMEIDIBI otandard, peptide,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          disorders such as psoriasis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example; Page 26; 42pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Feptides binding to the DNA binding domain of transcription factor and inhibiting cell cycle progression, useful for the treatment of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26 JAN 1000, 1000WC 6000127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      psoriasis; restenosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ,8021598;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ze JAN 1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DTA binding, transcription factor, EDF, EDF 1, cell bycle, DF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Paptide which binds to transcription factor E2F-1 DNA binding domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   905108W
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                                                                                                                                                                                                                                                                                                                            MVEMAE
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Cimilarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6 AA;
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                                                                                                                                   (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                         RESULT 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence is a polygluramine repeat domain binding peptide. Properties and expresses a protein having an expanded polygluramine region (og huntingtin), or atrophin 1, ataxin 1, 2, 6 or 7, or androgen receptor protein), or atrophin 1, ataxin 2, 6 or 7, or androgen receptor protein), or treating a neurodegenerative disease characterised by the presence of expanded polygluramine repeats, e.g. Huntington's disease, dentatorubral pallidoluysian atrophy (DRPLA), spinobubbar muscular atrophy, and spinocerebellar ataxia types 1, 2, 3, 6 and 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Huntington's disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New polyproprided which selectively bind to expanded polygiatamine repeat domains, useful for treating neurodegenerative diseases, e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mb1: Sous elesaciai
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14-MAR-2001; 2001WO-11508222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            W0200168678-A2
                                       08-DEC-1999;
                                                                                            08-JUN-2001
                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                          H11 binding site consensus conforming peptide (CCP) #2048
                                                                                                                                                                                                                                                                                                                                                             AAM45777 standard; Peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 13; Page 14; 59pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (UYDU ) UNIV DUKE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                spinobulbar muscular atrophy; spinocetebellar ataxia; noctropio
                                                                16661-JEG-1999;
                                                                                                                        CA2290722-A1
                                                                                                                                                                                                     cytostátic; vaccine; tumour specific immunogenic response inducer, astropytoma; fibroparcoma, myxosarcoma, liposarcoma, cligodendroglioma
                                                                                                                                                                                                                                  Antigen-kinding, turks, diagnosis, stress protein-peptide complex, SPPC, immunogenically cross-reactive; cancer; immunogenic cancer cell;
             (NOVO-) NOVOPHARM BIGTECH INC
                                                                                                                                                                                          epondymina,
                                                                                                                                                                                                                                                                                                                                                                                                                                    \leftarrow
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                    WKWWPF 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7 AA;
                                                                                                                                                                                          medulloblastima, primitive neural
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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                                       99CA-2290722.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Burke JP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 6, DB 22;
Pred. No. 7.8e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nagai Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                          estudermal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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AAR57399
ID AARS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Of protein-peptide complexes (SPPC) associated with tumours that is specifically immunogenically cross-reactive with cell surface ussociated CC specifically immunogenically cross-reactive with cell surface ussociated CC specs specific to target cancer (TC). Also described is an isolated CC antigen-kinding fragment if in antibody that kinds specifically to SPPCs CC antigen-kinding fragment if in antibody that kinds specific alone real CC surface-sesociated SPPC of TC (T) has cyrostatic activity and can be cused in vaccine production and as a tumour-specific immunogenic response CC inducer. (I) is useful for treating 71 types of cancers or tumours in a CC subject, such as astrocytoma, fibrosarcoma, myxosarcoma, liposarcoma, CC oligodendroglioma, pendymoma, medulloblastoma, and primitive neural CC ectodermal tumour (PNET). (I) is useful as cancer immunogen including CC ectodermal tumour (PNET). (I) is useful as cancer immunogen including CC vaccines. (I) is useful for diagnostic and palliative use, for detecting CC malignancy in an individual AAM4707 to AAM47109 represent poptidos which are used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Composition useful for treating and diagnosing cancer, comprise protein-peptide complexes associated with tumor, and isolated
                             Disclosure; Page 12; 14pp; Japanese
                                                                               A peptide and an adsorbing agent prepd. by immobilising it on a carrier—useful for treatment of diseases related to anti DNA
                                                                                                                                  WPI; 1994-260510/32.
                                                                                                                                                                                                     30-SEP-1992;
                                                                                                                                                                                                                                                                      12-JUL-1994
                                                                                                                                                                                                                                                                                                         JP06152290-A
                                                                                                                                                                                                                                                                                                                                                                          Carrier, absorbing agent, treatment, and i DBA and italy,
                                                                                                                                                                                                                                                                                                                                                                                                           Peptide for treating diseases related to anti-DNA antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-MAR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAR57399;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAR57399 standard; Protein; 8 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 4; Page 108; 154pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               antigen-binding fragments of an antibody that binds specifically to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Entwistle
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                                                                                                                                                                   (KURS ) KURARAY CO LTD
                                                                                                                                                                                                                                      18-JAN-1993,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 WRRWNF 6
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M, MacDonald GC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          invention describes a composition (I) comprising stress
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                     92JF-0261821
                                                                                                                                                                                                                                      93JP-0006098
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         , Score 6, IB
Pred. No. 7.86
3; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Dan MD, Lewis FE;
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The sequences given in AAR57386-413 are peptides which are

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AABC1498
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Best Local :
Matches
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Peptides which bind to the DNA binding demain of transcription
                                           Peptides binding to the DNA kinding and inhibiting well syste progression
                                                                                                                                                                                                                                                                      Misc-difference
                  Claim 4;
                                                                                                                                                                                                                                   Misc-difference
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                                                                                                                                                 26-JAN-2000: 2000WO-GB00227
                                                                                                                                                                                                                                                                                                                    Synthetic
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                                                                                                                                                                                                                                                                                                                                                                       Peptide which binds to transcription factor ECF 1 DWA Kinding 1 win
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RESULT 13
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The invention relates to compounds comprising a peptide chain all productly for 41 and 11 and 12 and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel compounds, useful for typating depressed neutrophil count, congrise postion chains of approximately for 40 minoral to be in that bind to grandle you colony original ting factor receptor.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 41; Page 67; 90pp; English.
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Z - OH or NH2; and \pi = 2-5. These peptides may be immobilised on a carrier in the preparation
                                                                                                                                                                             The sequences given in AARS7386 413 are peptides which are all covered by the claimed generic formula:
                                                                                                                                                                                                                                   Disclosure; Page 12; 14pp; Japanese
                                                                                                                                                                                                                                                                          antibodies
                                                                                                                                                                                                                                                                                         A peptide and in alsorbing agent parpl by immibilising it of carrier - useful for treatment of diseases related to anti-DNA
                                                                                                                                                                                                                                                                                                                                                 WPI; 1994-260510/32
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                                                                   X or Y are present;
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                                                                                                                                                            H-X-(A-B)n-Y-Z

    Mismatches

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                                                                                                                        protein, and so obtaining one or more inhibitory ligands; and (c) determining which of the inhibitory ligands can mediate a boological activity of the target protein. The present sequence represents a potential binding peptide for Haemophilus influenzae tyrosine tRNA synthetase from an example of the present invention. The method can be used for identifying drugs which can mediate the biological activity of a target protein. It can be used to identify the biological activity of a target protein whose biological function is not known and perhaps
                                cannot be determined directly. The method can also be used to identify new inhibitory ligands of specific target proteins. The method provides high throughput screens which are essentially identical for similar and dissibilar targets, typassing the need to develop distinct ascrys for biochemically diverse targets.
                                                                                                                                                                                                                                                                                                            A method has been developed for identifying a ligand which mediates the biological activity of a target protein (T) by inhibiting the binding of (T) to a binding partner. The method comprises (a) screening a first combinatorial library comprising first member ligands for binding to the target-binding ligands (TBLs), to identifying one or more TBLs; (b)
                                                                                                                                                                                                                                                                       screening a second library comprising second member ligands for the ability to inhibit the binding of the transfer of the TDIS to the farget
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                                                                                                                                                                                                                                                                                                                                                                                                                          Example 5; Page 100; 143pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Identifying ligands which mediate biological activity of a protein
by identifying target-binding ligands and screening a library for
ligands which inhibit target-binding ligand mediated activity
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library; inhibitory ligand.
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ALIGNMENTS

| RESULT 2 A71020 A71020 A71020 Lypothetical protein PH1454 - Pyrococcus horikoshii C.Species: Pyrococcus horikoshii C.Species: Pyrococcus horikoshii C.Species: Pyrococcus horikoshii C.Date. 14-Aug 1008 #sequence_revision 14-Aug 1008 #text_ubong. 20 II. 2000 C.Date. 14-Aug 1008 #sequence_revision 14-Aug 1008 #text_ubong. 20 II. 2000 C.Date. 14-Aug 1008 #sequence_revision 14-Aug 1008 #text_ubong. 20 II. 2000 C.Date. 14-Aug 1008 #sequence_revision 14-Aug 1008 #text_ubong. 20 II. 2000 C.Date. 14-Aug 1008 #sequence and gene utganization of the space of a lyget thempthia, No. Pyroth, A.Reference number. A71000, MUID.28344137, FMID.2679194 A.Rocession: A71020 A.Status. preliminary: nucleic acid sequence not shown, translation not shown A.Rocele type: DNA A.Rocele this accession replaces on interim accession for a separate replaced by 9:08 to 8. A.Gone: PH1454 | Query Match Pest Local Similarity 66 7%; Prod No. 1 Ben02; Matches 4, Conservative 2, Mismatches 6, Indelo 6; Saps 7; Qy 1 WXXWHF 6 [:: Db 26 WIVWHF 31 | RESULT 1 D70847 bypotherical protein Pv0n50 - Mycobacterium tuberculosis C.Species: Mycobacterium tuberculosis C.Species: Mycobacterium tuberculosis C.Pate: 17-Jul-1398 #sequence_revision 17-Jul-1338 #text_change 26-Jun-2500 R.Cole, S.T., Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S. Pajandream, Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harlin, N.; Halroyd, S.; Nature 393, 537-544, 1998 A.; Mathers 393, 537-544, 1998 A.; Math |
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RESULT 5
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7,600escion: 243876
A;Crops-references: GB:AE007869; PIDM:AAM86600.1; PID:g15155772; GSPDB:GM00169
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V6.15, Fred. Mo. 1.60-02,
Live C. Michaelle
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Field: No. 1.6e+02;
2; Micmatches (
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Science 294, 2317-2323, 2001
A;Authors You, H., Tur, Y., Biddle, F., Jung, M.; Krespan, W.; Perry, M.; Perdyn-Kamm,
eter, E.W.
A;Title: The Genome of the Matteral Graphic Stylings Agritation for timefactions for
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A;Map position: circular chromosome
C;Superfamily, site specific DNA methyltransferase (adenine-specific) Hpa1
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A;Accession: AD2674
A;Status: preliminary
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                                                                                                                                                                               A;Genome: nucleomorpn
C;Keywords: nucleomorph
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C;Genetics:
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A;Molecule type: DNA
A;Residues: 1-394 - POUS
                                                                                                                                                                                                                                                                                                                                                                                A;Title: The highly reduced genome of an enslaved algal nucleus A;Poference number: AqqQq2; MUD:11323671; PMID:11323671 A;Accession: 090105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   putative SAP DNA binding protein: [imported: Gillardia then surleaming C;Species: nucleamorph Guillardia theta
A;Note: a nucleamorph is the vestigial nucleus of a cukaryotic endosymbiont C;Dare: 10-May:2001 #soquencq_revision 10-May:2001 #sax=_thange 24 May 2001
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A; Residues: 1-386 < KUR>
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CySpecies: Agrobacterium tumefaciens
CyDate: 11 Jan 2002 #teoguenoc_rovision 11-Jan 2002 #text_change 17-May-2002
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Nature 410, 1091-1096, 200
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                                                                                                 Matches
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     169 WYSWHF 174
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4. Ocnobry
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Pred. No. 1.7e+02;
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       C;Species: Listeria innocua
C;Dato: 07.Nov.2001 #sequence_revisits 27 Nov 2001 #tbXt_chinge 14.Dro-2001
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C;Accession:
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                                                                 PTS system galactitol-specific enzyme IIC component homolog linnel4 (imported)
                                                                                                                RESULT 12
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A,Experimental source, Strain EGD-e
C.Genetics:
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C.Date: 27-Hov 2901 #sequence_rwvision 27 Mov 2011 #text_change 14 Nov. 201
C;Accession: AH1407
R,Glaser, P., Franzeyl to messer
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A;Title: The genome sequence of the facultative intracellular pathogen Brucella mod. Const. A;Reforence number: AD3252; PMID:11756688
                                                                                                                                                                                                                                                                                                                               A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1:423 <GLA>
A;Cross:references: 38:1
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A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; ok, C.; Schlueter, T., Simoes, N.; Tierrez, A.; Vazquez EA;Title: Comparative genomics of Listeria species.
A;Feference number: AB1077, MrHz 21517277, FXIT 11673669
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C;Superfamily: site specific DNA methyltransferase (adening
T;Feywords methyltransferase, 2 whole;)methionine
                                                                                                                                                                                           A;Gene: lmc2665
C,Superfamily, phosphotransferase enzyme II galactitol specific
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CyDare, 0. Fet 1990 #sequenno_revision of Feb 2000 #Fext_change 17 May 2002
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A; Residues: 1-403 < KUR>
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126 WNYWHF 131
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                                                                                                         h looto8; Score 38; DB 2; Similarity 66.7%; Pred. No. 1.8e+02; 4, Conservative 2, Mismutches 3
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Bernal, G.; Duchaud, E.; Durand, L.; Dussurger, O.; Enrian, K.D.; E
M.; Karst, U.
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Boland, J.A., Voss, H., V
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compa-6 desaturase, Chloroplast - soybean
C/Species: Glycine max (soybean)
C/Species: Glycine max (soybean)
C/Species: In May 1999 #roquence_recorden 14 May 1999 #text_change 08 Oct 1999
C/Accession: T07742
R/Hitz, W.D. Tiller, T.T., Proth. J.F., Fisher, A.T., Thorn, F.L., Tiller, N.S.
Plant Physiol. 105, 635-641, 1994
A/Fitle: Cloring of a higher-plant plastid exega-6 facty acid desaturase cDNR and its ex
A.Reference number: Z16109; MIID:94345008; PMID:8066133
A/Accession: T07742
A/Molecule type: mRNA
A/Residues: 1-424 <HIT*
A/Coss references: EMBL:129215; NID:9459961; PIDN:A/AA60159:1; PID:q489962
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A.A.Thur. Kaves, J., Kuhi, M., Kini, F., Kiraphat, G., Midadin, E., Millington, A., M.
A.A.Thur. Kaves, J., Kuhi, M., Tierrez, A., Varquez Boland, J.A., Voss, B., Wehland,
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A)Genetics:
A)Genetics:
C)Gujetfatty ordereductase
C)Keywords: chloroplast; oxidoreductase
E)1-40/Gomin franci popido (hibrarian) #ciarus grodirod
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GrSpecies: Chlamydomonas reinhardtii
GrDate: 18.Mar-1998 #sequence_revision 18-Mar-1998 #text_change 20-Jun 2700
GrAccession: JC5891
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C:Superfamily: phosphotranofotase enzymo II gulautitul-specific
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.; Domingwez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.;
D.; Jones, J.M.; Karst, U.
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eurosids I: Fabales; Fabaceae, Papilionoideae; Phasecleae; Clycine
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Omega-6 fatty acid desaturase, chloroplast procursor (EC 1.14.99.).
Glycine max (soybein)
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ProDom; PD001081; FA_desaturase; 1
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Hitz W.D., Carlson T.J., Booth J.P. Jr., Kinney A.J., Steeda K.L.,
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Spermatophyta, Magnoliophyta, eudicotyledins,
eurosids II; Brassicales, Brassicaleae, Arabi
NCBI_TaxID=3702;
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01-NOV-1997 (Rel. 35, Last sequence update)
15-JUN-2092 (Pel. 41, Last annotation update)
Hypothetical protein At5927120
AT5927120 OF TM921894 12 OF T0184 10
                                                                                                                                                                                  EMML; AP007271; AAB61073.1; -.
Interpro, IPP0072647; Nop
Pfam; PP01798; Nop; 1
Procom, PD014104; Nop; 1
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-!- SIMILARITY, BELONGS TO THE NORS/NORSE FAMILY.
                                                                                                                                             Hypothetical SEQUENCE 4:
                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PPOT entry is copyright. It is produced the EMPR outstation between the Swiss Institute of Bioinformatics, and the EMPR outstation.
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Brassica napto (Rape).
Bokanyina, Mildiplantas, Streptophyta, Enkryiphyta
Spennarophyta, Mildiplaphyta, e.eli tryindras, tr
eurosids II; Brassicales; Brassicaceae; Brassica
NCBI_TaxID=1708;
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01-FEB-1996 (Rel. 33, Last sequence update)
15-UCM-2002 (Rel. 41, Last annotation update)
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RX MEDILINEAU COMMINGENCY (1988)

RX MAYOR R.F.M. Schwelle: C. Warthit F. Vergy, C. Terryn N. Mayor R.F.M. Schwelle: C. Warthit F. Vergy, C. Terryn N. Mayor R.F.M. Schwelle: C. Warthit F. Vergy, C. Terryn N. Mayor R.F.M. Schwell: L. Reger M. Maller M. Fahler S. Martin F. Maller M. Schwell: L. Reger M. Maller M. Fahler S. Maller M. Schwell: L. Reger M. Maller M. Schwell: L. Reger M. Maller M. Schwell: P. Maller M. Schwell: T. Reger M. Maller M. Schwell: P. Maller M. Schwell: T. Reger M. Maller M. Schwell: P. Maller M. Schwell: T. Reger M. Maller M. Schwell: P. Maller M. Schwell: T. Reger M. Maller M. Schwell: P. Maller M. Schwell: T. Reger M. Maller M. Schwell: M. Maller M. Schwell: M. Maller M. Schwell: M. Schwell: M. Maller M. Schwell: M. Maller M
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Arabidogeis chaliana (Mouse-ear Crees)
Enharyttu, Viridi, Inclae, Creepingbyta, Embryophyta, Trac
Opermutchhytu, Majoclich)tu, ordinatyledono, corocadico
Perrosids II. Brassicales, Brassicaceae, Arabidopsis.
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               Shinadaki E., Paris P.W., Bakat J.B., Theologia A., "Rizer A. Labidapois full sequesion della clares (RMTIS) sequesion della calculation (Salk/Slanfavil/PSEC).";

Calculation (GET-1871) to the EMST/PSECANT della threes
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Uta; Andinstyledons, coroleddicoto, Rocidae
Brassicaceae; Arabidopsis.
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lenes (RAFIs) sequenced by the
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MEDLINE=98019091; PubMed=9358059;
Kim Y C., Miller C.D., Anderson A
                                                                                                                                                                                                                                                                                                                                           Q59714;
30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
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EMBL; AL161578; CAB79813.1; ...
EMBL; AV045621; AAK73979.1; ...
EMBL; AV058078; AAL24186.1; ...
EMBL; AV059852; AAL24186.1; ...
InterPro; IPP001225; FA_desaturase.
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                                                                                                                       Fim Y C , Miller C D , Anderson A J.; "Identification of adjacent genes encoding the major bacterioferritin from the plant-beneficial bacterium
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Oxidoreductase; Fatty acid biceynthesis, Chloroplast, Membrane,
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     -!- ENZYME RECHLATION
                                                                                                                                                                                                              SEQUENCE FROM N.A.
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                                    PROTICE DECOMPOSES HITEORED REPOXITE IN WATER AND EXPRESS TO PROTECT CELLS FROM THE TOXIC PEPECTS OF HYDROGEN PERCYICE CATALYTIC ACTIVITY: 2 \cdot H(2) \circ (2) - \circ (2) + 2 \cdot H(2) \circ.
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                       COFACTOR: HEME GROUP
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HISTIDINE BOX-3.
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R InterPro; IRR00122.,
R InterPro; IRR00122.,
R Fism; PFC0199, Catalase, 1.
PR Fism; PFC0199, Catalase, 1.
PR FRUNTS; PRC0067; Catalase; 1.
PR PROSITE; PS00438; CATALASE 1; 1.
PR PROSITE; PS00438; CATALASE 2; 1.
PR PROSITE; PS00438; CATALASE 1; 1.
PR PROSITE; PS00438; DATALASE 1; 1.
PR PROSITE; PS00438; DATALASE 1; 1.
PROSITE; PS0438; DATALASE 1; 1.
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CHAPACTERIZATION, AND MUTAGENESIS.

MEDILINE-19038777; PubMed-19172949),

Bactier T., Bergus T., Tulleivey D., Hurt E.;

"Mocloslar KKE/D repeat groteins Regist and Mogleg interact with Mopip

"Mocloslar KKE/D repeat groteins Regist and Mogleg interact with Mopip

and are required for ribosome biogenesis.";

Mol Cell Riol 17 7088-7088 (1805)MAI SHRUMIT SYNTHESIS.
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SIKI OR NOP56 OR YER197W OR L8167.9.
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Eukaryota, Pingi; Ascomycota, Saccharomycotina, Saccharomycetes;
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HSSF, F42321, 2CAE.
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M->R: REPUGED GROWTH RATE AT TEMPERATURES, WHEN ASSOCIATES
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Interactio, IERNOVAGE, Mop.

E Fiam, FF01708, Mop; 1.

DR ProDom, P0004104; Nop; 1.

DR ProDom, P0004104; Nop; 1.

ASP/GLU/LYS.RICH.

ASP/GLU/LYS.RICH.

LELYCH F
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Gayarar, Gaross, Gauden)

16 companyol (Rel. 40, Orested)

16 companyol (Rel. 40, Last segmence update)

17 rmy 2000 (Rel. 40, Last amontation update)

17 rmy 2000 (Rel. 41, Last amontation update)

17 rmy 2000 (Rel. 41, Last amontation update)
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Submitted
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      17
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Eukaryota, Metazoa, Cherketa, Craniata, V
Mammalia, Eutheria, Primates, Catarrhini,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID-9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SPÉDENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bloecker H., Boecher M., Brandt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM W.A.
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                                                      TISSUS SPECIFICITY: Chiquitous.
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lation and characterization of a newel
potential (2007).
      TORG-SSIWS
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ing and characterization of
tied (JAN-1999) or the FMSL
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//GenBank/DDBJ
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   is fraduced
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between the Swiss Institute of Bioinformatics and the EMBL outstation

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          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the Furopean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this starement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                             SEQUENCE FROM M.A. SECURING OF 1.20, AND INTERACTION WITH MODOL MEDILING COLD ASSOCIATION. FLEMAL 10679015;
YANG Y. I BRANC C. WAND C. DEAGON F. POGRACIO V. Moder U.T.;
"Conserved composition of marmalian box H.ACA and box 0/5 cmall nucleolar ribonucleoprocein particles and their interaction with the common factor Noppla0";
Common factor Noppla0";
Mol. Biol. Cell 11.507 597 (2000).
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16-00T-2001 (Rel. 40, Created)
16-00T-2001 (Rel. 40, Last sequence update)
15-JMN 2002 (Rel. 41, Last annytation update)
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                                                                                                                                                                                                                                                                                                                                                                                                             Pattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vortebrata; Euroloostomi;
Mammalia; Eurberia: Podontia; Solurognathi: Muridae; Murinae; Pattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein)
NOPS OF NAP65
                                                                                                                                                                             Hatton D., Gray J.C.;
Submitted (JUN 1998) to the EMBL/GenBank/DDRJ databases.
-!- EUNCTION- REGULEED FOR FOS PIROSOMAL SUBJULT BIOGENESIS
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entities requires a license agreement (See http://www.isb-sib-ch/announce)
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                                                                                                              SIMILARITY: BELONGS TO THE NOPS/NOPS6 FAMILY.
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AF26460R; AAF91394 1; ...
AL117554; CAB55989 1; ...
AF164469; AAE29094 1; ...
S5.2DFAGE; Q9YZX3; HUMAN.
BYPTO, IFROCZ687; Ny
                                                                                                                                                               similarity).
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RESULT 14
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Best Local :
                                                                                                                                                                                                                  EMPL, ABODOPET, AAB91634.1; -. Interpr., IPRO20157, TIE Jomain. SMART; SMO0255; TIR; 1. SMART; SMO0255; TIR; 1. Hypothetical protein, Plasmid. BYTHEFORTHARACTE TETR4; SEQUENCE 646 AA; 71609 MW, BYTHEFORTHARACTE TETR4;
                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PPCT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMED colstation the European Bioinformatics Institute. There are no rectricities on its use by non-profit institutions as long as its nutset is to ensure way modified and this statement is not removed. Happe by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/er-send an email to licenselish sib.ch).
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01-NOV-1997 (Fel. 36, Last seglement
01-NOV-1997 (Rel. 35, Last annotati
Hypothetical 71.6 kDa protein Y4CD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Molecular basis of symbicsis between Rhipobium and legumes."; Nature 387 394 401(1997).
! SIMILARITY, NONE OBVIOUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-97305956; PubMed-9163424;
Freiberg C A , Fellay B , Bairoch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria, Froteobacteria, alpha subdivision, Phizobiaceae group;
Phizobiaceae; Phizobium
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EMBL; AF069782; AAC23535.1; -
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Pibosome biogenesis, Nuclear protein.
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521 WPFWHP 526
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Pred. No. 84;
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EMEL, AR229397; AAKCOCK.

InterPro, IRRO1025; FA_decaturace.
Pfam; PD0107; FA_decaturacy 1.
ProDom; PD010R1; FA_decaturacy 1.
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090600; PRELIMINARY; PRT; 201 AA.
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01-3UN 2001 (Tremburel 17, Lust sequence up
01-3UN 2001 (Tremburel 17, Lust sequence up
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Q96N05 (TrEMBIrel 19, Created)
01-DEC-1001 (TrEMBIrel 19, Last sequence update)
01-DEC-2001 (TrEMBIrel 19, Last sequence update)
01-DEC-2001 (TrEMBIrel 19, Last amoutation update)
01-DEC-2001 (TrEMBIrel 19, Last amoutation update)
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Buranjina, Tiridiplanta, Oiregriph, N. Pilip physa, Tiridi physa,
Spermarophysa, Maganolichybra, eddicotyledons, core cudicots, Rusidae,
eurosids II) Brassicales, Brassicaceae, Arabidopsis.
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Prepryst, Mrizza, Christa,
Mammallu, Eutheria, Primates,
NoBI_Tu-IT offi.
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156 WVNWHF 161
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nes 4, Conserv
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66.7%, Field. No. 2e+1
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CC.71, Bied. W., live
tive 2; Mismatches
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Cutarrhini, Buminidae,
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STRAIN-TV BROWN;
Evaluation M., Proger N., Brunel D.;
"Amplified consumous judy malkers T.
"Amplified consumous function genes in
Life EMEL J. AEMONG function genes in
Life EMEL J. AEMONG function
EMBL; AF229390; AEMONG for desaturate.
Pfam; Provide/; PA_desaturate; 1.
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Q9AXY3;
01-JUN-2001
01-JUN-2001
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FILLE IN., FILDER W., Brinel C.,

Amplified Conscious gave markets Tucks decig

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EMBL, AFLESSER, AAKOUSSOLI; -.

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01-JUN 2001 (TrEMBLrel. 17, Created)
01-JUN 2001 (TrEMBLrel. 17, Last sequence update)
51 JUN 2002 (TrEMBLrel. 21, Last sequence update)
7-cj. f.t.d...tase (Fragment).
FAD6-BN-2.
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Erkarytta, Whilliplantae, Erreptiplo, Erktyppio, Trackophyter
Spermatophyta, Majorlippiyla, eudicotyledons, core eudicots, Rosidee,
eurosids II, Ersesicales, Brassicaceae; Brassica.
MTMI Trwib:2711;
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Spermitsphyta, Majaclisphyta, e.dionyledono, once endicota, R
eurosids II, Brassicales, Brassicaceae, Brassica.
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66.7%;
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2, Midmatches 0,
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PUT 01-UEC-2001 (TrEMHLES) 19, Last sequence update)

DT 01-UEC 2001 (TrEMHLES) 21, Last annotation update)

DT 01-UN 2000 (TrEMBLES) 21, Last annotation update)

DE Putative 6-phosphogluconolactonase

Arabidopsis thaliana (Mouse-ear cress)

OR Arabidopsis thaliana (Mouse-ear cress)

OR Enkaryota; Viridiplantae: Stroptophyra, Embryoghyra; Trathoghyta;

OR Spermatophyta; Magnoliophyta, Audicotyledons; Internations; Ensider;

OR eurosids II, Brassicales; Brassicaceae; Atabidopsis.
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                                                                                                                               Yamada K. Liu S.K. Sakano H. Pham P.M. Paph J. Ching M.M. Goldsmith A.D. Lee J.M. Quach H.L. Tang C.C. Toriumi M. Yu G. Bowser L. Carninci P. Chen H. Oheuk P. Hayashiraki Y. Ishida J. Jones T. Kamuya A. Karlin-Neumann G. Kawai J. Kim C. Kosema E. Lam B. Liu J. Meyers M.C. Miranda M. Sayusaka M. Nguyen M. Echem B. Liu Sakurai T. Sarrou M. Seki M. Shinn P. Southwick A., Shinnraki Y. Davis P.M. Ecker J.E. Theologis A. Southwick A., "Full Length CDNA of gene KIGHJ 11/AT524400 (GI 1017701) "; Submitted (ARR-2001) to The EMBL/GenHank/DBH databases -- SIMILAPITY CRUANIC 1 WD FEIBAT (TEF ASF 20MAII).
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01-JUN 2001 (TrEMRLrel 17, Created)
01-JUN 2001 (TrEMRLrel 17, Last sequence update)
01-JUN-2002 (TrEMRLrel 21, Last annotation of date)
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Eukary-ta, Viridiplan
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216 AA;
                                                         repeat.
219 AA;
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Score 39,
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DB 10,
                                                         CROK4,
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Length 219
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RY STRAILHEARY,

RY MEDLINE,9829587; FubMed-9634236,

RX MEDLINE,9829587; FubMed-9634236,

RA Cole S.T., Brosch R., Farkhill J., Garnier T., Churcher C., Harrin D.,

RA Cole S.T., Eighmeier K., Gas S., Barry C.E. III, Tekaia F.,

PA Gordon S.V., Eighmeier K., Gas S., Barry C.E. III, Tekaia F.,

PA Gordon S.V., Eighmeier K., Cas S., Hamlin H., Holley G.,

RA Davies R., Jevlin K., Foltwell T., Gontles G., Hamlin H., Holley G.,

RA Hornsby T., Jayels Y., Frogh A., McLean J., Moule S., Murphy L.,

PA Oliver S., Oshorne J., Chail M. A., Rajandream M. A., Pogers J.,

RA Rutter S., Seeger K., Skelton S., Squares S., Squares R.,

RA Suls:on J.E., Taylor E., Whitehead S., Harrell H.G.,

PT "Deciphering the biology of Mycobacterium tuberculosis from the

RT Complete genome sequence.";
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ProDom; PD00108
MON_TER 1
MON_TER 222
SEQUENCE 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                   053604;
053604;
                                                                                                                                                                                                                                                                                                                                                         01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
61-MAR-2002 (TrEMBLrel. 09, Last annotation update)
Hypothetical protein Rv0059.
FV0650 GF MTV000 02 OP MT0065.
                                                                                                                                                                                                                                                                                                        Mycobacterium tuberculosis.
Bacteria, Firmicutes; Actinobacteria,
Actinomycetales, Corynebacterineae, M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fourmann M., Friger N., Brinel D., "Amplified consensis gene markers. The sidesigning for a genetic of Arabidopsis-known-function genes in Brassica."; Submitted (JAN-2000) - the EMBL/SenBark/DDBJ databases.
EMBL, AF229399, AAK00661.1; -...
InterPro; IPR001225; FA_desaturase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta, Spermatephyta, Magneliophyta, eudicotyleduns, core eudicots, Rosiceurosids II; Brassicales; Brassicaceae; Brassica.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JUN-2001 (TrEMBLrel. 17, Created)
01 JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 11, Last armotation update)
01-JUN-200 (TrEMBLrel. 11, Last armotation update)
0mega i reductase (Fragment).
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PD001081; FA_desaturase; 2.
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Lear J. MW;
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O59123,
O59123,
O1-AUG-1998 (TEMBLIFE), O7, Created)
O1-AUG-1998 (TEMBLIFE), O7, Last Seque
O1-AUG-1998 (TEM
Q9FIN2;
Q9FIN2;
01 MAR-2001
01 MAR 2001
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Fleischmann F. T. Alled D., Eisen T.A., Teperer I., White T.,

Peterson J., Deby E., Eds.L.B., Caken M.L., Haft E., Hilber E.,

Kolonay J.E., Mels H. W. T., Thy M. N., Freilberg M.E., Calebry J.L.

Belehe A., Utterback T., Weldman J., Khouri H., Gill J., Mikula A.,
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Hypothotical gritein,
SeCUENCE 230 AA:
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Submitted (APR-D01)
EMBL, ALC21428, CAA16240.1;
EMBL, AE006919, AARHICST.1,
TIGR, MT0065;
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MEDLINE 98344137; PubMed 9679194;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
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othorical protein, Complete proteins
TERTE off AA, 2014 MM, A TOTIFAIETTEIS
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Last sequence update
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Best Local:
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Best Local
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DIRAIN CO
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"Obtactiff analysis of Arabidaguis challand observations to be appeared for the regions of 1,000,000 by overed by physically accided by and TAC clones.";

EMA Res. 0.300-391(1998).
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6-phosphoglucosciactomace like protesin.
AtabioSpsis thaliana (Mouse-Pricress)
Eakary-ta, Virial Juntae, Streft Libyta, Enlay-phyta, Trachocybyta;
Cremer, byta, Majorit (byta, Audion, Louis audions, Bosidae)
waruside II, Braceius'ee, Fressi (More, Archibets,
WIET_TART (1792)
                                                                                                                                                                                                                                  Science 281:375:388(1998),
EMEL; AECOLDO; AACCED08.1;
TIGE; TROCCL; -
TIGE; TROCCL; -
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COMMON R., GALLEY E.K., Clayers M., Fertalia R., Fertalia R., Sedergien E., Hardham J.M., Moteral M.E., Gallebaug S., Fertalia R., Sedergien E., Hardham J.M., Moteral J.K., Callebaug S., Fertalia R., Ditterback T., Moteralia R., Fertalia R., Fertalia R., Sedergien E., Hardham J., Sewell J.K., Cotton M.D., Fujii C., Garland S., Moteralia R., Fertalia R., Sandusky M., Weidman J., Smith H.O., Harth B., Hotet E., Butwith E., Sandusky M., Weidman J., Smith H.O.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDINE 33156233, FubMed-10048488;
Appelot 6 , Str. 3 , Establis T , Nikemini V
                                                                                                          SEQUENCE 260 AA;
                                                                                                                                                                                                                                                                                                                                               Venter J.C.;
"Ouglete genere requence of Treporers pallidum,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID-160;
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Bacteria; Spirochaetales;
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PRODITE, FS00022, EGF_1, THENOWN_1.
Cuth_n,pept.date, C_flite protoume.
SEQUENCE 260 AA, 29193 MW; EB5601245133BE56 CRC64;
                                                                                                                                                                                                              InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ESTRUCE ESTABLES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TRAIN-NICHOLS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               72 WARWHF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WXXWHF 6
                                                                                                                                                                                                                                                                                                                                                                                                       H G ()
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COLUMBIA;
     Similarity 66.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cimilarity 66.7
                                                                                                                                                                                                                    IPR003709;
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                           100.0%;
66.7%;
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                                                                                                                                                                                                                                                FGF-like
pred. No. 2.5e+02;
2; Mismatches 0;
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2, Mismatches 0,
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RESULT 14
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Best Local
  SEQUENCE FROM N.A.

STRAIN-APTC 15692 / PAO1;

MEDDINE-2043737; PubMed=10984043;

MEDDINE-20437337; PubMed=10984043;

Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P.

Hickey M.J., Brinkman F S.L., Hufnagle W.O., Rowalik D.J., Lagrou
Garber P.L., Goltry L. Toleptino E, Westbrock Waddman S., Yuan Y.

Rrody I.L., Coulter S.N., Folger K.P., Mas A., Larbig M., Lim P.M.

Rrody I.L., Spencer D., Woong G.K. S., Wu Z., Paulsen I.T.,

Reizer J., Saler W.H., Hancock P.E. W. LOTY S., Olson M.V.;

"Complete genome sequence of Pseudomunas aeruginosa PAO1, an

opportunistic pathogen.";

N.11774 Audit Advanced (June)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AE010783; AARMUNDO...;
Hypotherical procein; Complete proceeme
SEQUENCE 290 AA; Piped MW; E4201708
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Galagan J.E. Mubbaum C. Roy A., Endriczi M.G., Macdonald P., Firthigh W., Calvo S., Engels R., Smirnov S., Atnocy D., Brown A., Allen N., Mylort I., Stange Thomann N., DeArelland Y., Johnson P., Linton I., McEwan P., McForman Y., Talamas J., Tirrell A., Ye W., Zimmer A., Barbor P.D., Cann I., Graham D.E., Grahame D.A., Guss A.M., Leigh J.A., Li W., Liu J., Mukhopadhyay P., Reeve J.N., Smith K., Springer T.A., "Mayam I.A., Whire O., White P.H., de Macario E.C., Springer T.A., "Mayam I.A., Whire O., White P.H., de Macario E.C., Springer T.A., "Mayam I.A., Whire O., White P.H., de Macario E.C., Springer T.A., "Mayam I.A., Whire O., White P.H., de Macario E.C., Springer T.A., "Mayam I.A., Whire O., White P.H., de Macario E.C., Springer T.A., "Mayam I.A., Whire O., White P.H., de Macario E.C., Springer T.A., "Mayarm I.A., Whire O., White P.H., de Macario E.C., Pritchert M., Sowers K.P., Swanson P.V., Zinder E.H., Jander E., Willey B., Swanson P.V., Zinder E.M., Scholley B., Swanson P.V., Zinder B., Scholle
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01-JUN 2002 (TYEMBLYG)
01-JUN 2002 (TYEMBLYG)
                                                                                                                                                                                                                                                                                                                                                                                                                        Hypothetical protein PA2778
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. SERRE / DRM CR24,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAR 2001 (TrEMBLIFE)
01-JUN 2002 (TrEMBLIFE).
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01-MAR-2001 (TrEMBLre)
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Genome Res 12:532:542(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-21929760; PubMed=11932238;
Galagan J.E., Nusbaum C., Roy A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Methanosarcinaceae;
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Nature 406:959-964(2000).
                                                                                                                                                                                                                                                                                                                NCBI_TaxID=287;
                                                                                                                                                                                                                                                                                                                                                              Bacteria; Protechacteria; gamma subdivision; Pseudomonadaceae;
                                                                                                                                                                                                                                                                                                                                                                                              Pseudomonas aeroginosa
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21, Dast seguence up
21, Dast annotation
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16, Cast sequence update)
21, Last annotation updat
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Search completed. February 20,
Job time . 25.3333 secs
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Best Incal
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01 MAP-2001 (TYEMBLYE] 16, Cypated)
01-MAP-2001 (TYEMBLYE] 16, Last sequence update)
01-200-2002 (TYEMBLYE], 21, Last annotation update
01-200-2002 (TYEMBLYE], 21, Last annotation update
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InterPro, IPP005074; Peptidase_C39,
InterPro, IPR001440; TPR
Pfam; PF03412; Peptidase_C39; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Saklani-Jusforgues H , Fontan E , Goossens P.L.;
"Characterisation of a Listeria monocytogenes mutant deficient
arabitol fermentation.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Listeria monocytogenes.
Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUN-2002 (TrEMBLiel, 2), Last annotation update)
Putative phisphotransferase D arabitil specific component IIO
                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Res. Microbiol. 152:175-177(2001).
EMBL, AJ292552; CAC20641.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Listeriaceae, Listeria.
NCBI_TaxID=1629,
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Pfam; PF03611, EIIC-GAT; 1.
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                                                                                                                                                                                                                                                                                                  Match
Local Similarity 66.7%;
                                                                                                                                      JIIMANA 8T
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310 AA,
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                                                                                                                                                                                                                                                                     2; Mismatches
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                                                                                                                                                                                                                                                                                                  Score 18; DR 2; Length 310;
Pred No 3e+02;
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Post-processing: Minimum Match 0%
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Maximum DB seq length։ շոնդոնդնձը
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Total number of hirs sarisfying chosen parameters:
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1: /GIDSC/g-gdata/g-
2: /GIDSC/g-gdata/g-
3: /SIDSC/g-gdata/g-
                            10:
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12:
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38
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                                        Peptides which bind to the DNA binding domain of transcription factor ESF and inhibit cell cycle progression may be useful as feeder to the second of the second feeder for add DP-1, or the activation to investigate the interaction leaves ESF and DP-1, or the activation of transcription by ESF-1/CET invest. They may be seen for it links in French 10. The process in a cell, particularly for presument of cancer or other proliferative at cell, particularly for presument of cancer or other proliferative.
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30-JUN-2000; 2000US-0608408
03-AUG-2000; 2000US-042366
21-SEP-2000; 2000US-0234687.
27-SEP-2000; 2000US-0236359.
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                                                                   Single exon morteic arid probes for analyzing gene expression in human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  09-AUG-2001
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epilepsy; cancer.
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                                                                                   The present invention privides a number of hingle even number said probes which are derived from general sequences expressed in the human bone marrow. They have be used to be useful expression in home marrow samples, which may enable the improved dispussion and treatment of correct coch as lymphoma, loukachia and myoloma. The present acquence is a protein encoded by one of the probe of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia, epileps, and danters. The present sequence is a protole enoughly one of the invention
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The propert invention relates to single each nucleic hild probed (CENF) see ANT31315-ANT57546). The present sequence is a peptide encoded by one cath probe. The problem are useful for probleming a minimum property for probleming and displaying gene expression in surples derived from human procents. The problem are useful for untenstal displaying for human genetic disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human genome-derived single each modeic acid probes useful analyzing gene expression in human placenta -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Reptide #8700 ensoled by probe for measuring placental gene expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mi_roarray, human, placenta,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MODECULAR DINAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQ IL NO SAMBL; 654pp; English
100.0%; Score 38; DE
Ac.C3; Etcl: N. 56;
Coe C, Micratches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              untenatal diagnosis;
                                                                            DB 22;
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                                                                                                                                                                                                                                                                                                                             ABG64892
                                                                          RESULT
                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                          Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                              acids may be used to produce the polypoptides, by inserting the nucleic acid and its complementary sequences may also be used as DNA probes in diagnostic assays to detect and quantitate the presence of similar nucleic acid and its complementary sequences may also be used as DNA probes in diagnostic assays to detect and quantitate the presence of similar nucleic acid sequences in namples, and therefore which patients may he in need of restorative thorapy. The proteins may also be used as antigens in the production of antibodies against bone marrow proteins and in assays to identify modulators of their expression and activity. The antibone marrow protein antibodies and antagonists may also be used to down regulate expression and activity. The antibales may also be used as diagnostic agents for detecting the presence of the protein in samples
                                                                                                                                                                                                                                                                                                                 (e.g. by enzyme linked immunosorbant assay (ELISA)) The proteins may be used to regulate haematopolesis activity, and consequently in the treatment of myeloid or lymph cell disorders; in tissue regeneration, such as wound healing; as a nutritional supplement; and in treatment of immuno disorders such as severe combined immunodoficiency (SCID).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pone marrow, diagnostic; therapeuric; gene therapy; antigenic; haematopolenis; myeloid; lymph cell disorder; tissue regeneration; wound healing; nutritional supplement; immune disorder, severe combined immunodeficiency; SCID.
ARCK4892;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAU14602-AAU14794 represent novel bone marrow polypeptides of the invention. The proteins and corresponding coding sequences may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate bone marrow polypeptide expression. For example, to treat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and gene therapy
                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   or deletions in a patient's genome that affect the activity of the polypeptides by expressing inactive proreins or to supplement the patient's own production of the polypeptide. Additionally, the nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 10; Page 248; 392pp; English.
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20 JUN 2000; 2000US-0598075
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                                  ABG64892 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           disorders associated with decreased expression by rectifying mutations
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30-NOV 2000; 2000US-0550683
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                                                                                                                               14 WLIWHF 19
                                                                                                                                                                                                                            Local Similarity
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RESULT 11
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention relates to alturin fusion proteins comprising a therapeutic protein X and human albumin (HA, also known as human serum albumin, HSA). The proteins are useful for treating a disease or disorder that may be modulated by therapoutic protein X. The albumin extends the shelf-life of protein X, and may increase its biological in vitro/in vivo activity. The protein is useful for treating and diagnosing disorders such as cancer, reproductive disorders, disease, observe colitis), inmune disorders (e.g. acquired immunodeficiency syndrome, AIDS), endocrine disorders (e.g. alabetes), haematopoletic disorders, neural disorders (e.g. Alzheimer's, Parkinson's, Creurzfeld-(arob disease, encephalumylitis, meninglitis, subliciphicula), and connective disorders (e.g. osteoporosis, arthritis). ABGS3325-ABG65518 represent albumin
Human gene 18 encoded secreted protein HNNBM45,
                                                                                                          01 JUL-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New fusion protein for treating disease e.g. diabetes comprises albumin fused to a therapeutic protein - % \left( 1\right) =\left\{ 1\right\} =\left
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rosen CA,
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25 AFR:2000; 2000US-199384P.
21 TET:2000, 2000US-25697F
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                                                                                                                                                                                                                    AAE21233;
                                                                                                                                                                                                                                                                                                                        AAE21233 standard; Protein; 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18 OCT-2001
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66.7%; Pred. No. 81;
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SEQ ID NO:98
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AADJ3022 NUB3770 regressed LEMAS ilregereding to 21 human secreted CC AAE2223 AADJ312 regressed toward the private they recall to AAE2223 AAE2223 regressed toward the private they recall to AAE2223 regressed toward the private they recall to AAE2223 regressed graveling are useful for preventing and and their corresponding secreted graveling as useful for preventing to another regression of their regression regression of their regression re
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Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Misc difference
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/label= Signal_poptide
32..53
/label= Mature_secreted_protein
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vaccinating against and diagnosting infections, especially useful
treating arms valgaris.
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         disorder in humans, and in the manufacture of a medicament for treating a syndrome associated with open isociated disorder. Open polynopleotide sequences can be used in the reatment of cancer, hyperproliferative disorders, cirrhosis of liver, psoriasis, benign tumours, keloid, degenerative disorders, haemorrhage, ostecarthritis, neurodegenerative disorders, disorders related to organ transplantation, cardiovascular diseases, diabetes mellitus, systemic lypus erythematosus, hypertension, hypothyroidism, cholesterol ester storage disease, various immune deficiences and disorders, infectious diseases, autoimmune disorders such as multiple sclerosis, rhematoid arthritis, autoimmune thyroiditis, myasthenia gravis, graft-versus-host disease and autoimmune inflammatory eye disease. NETX proreins are also tesful for treating hyper incience allocated to the control of the 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human: Open reading frame; ORFX; gene therapy; cancer; cirrhosis; hyperproliferative disorder; psoriasis; benign tumour; haemorrhage; dogenorative disorder, estecarthritis, neurodegenerative disorder; ardiovascular disease, diabetes mcllitus; systemic lupus elythomatosus; hypertension; hypothyroidism, cholesterol ester storage disease, immune deficiency; immune disorder, infectious disease.
                                                                                                                                                                                                                                                                                                                                                                                  The present invention describes substantially purified human proteins (referred to as open reading frame, ORDANCE I 1-11491 (see Table in the specification) APRISTAC TO ARRIETSS encode the human ORFX proteins given in ARREDOULD to ARRIETSO. ORFX proteins are useful for treating or preventing a pathology associated with an ORFX-associated treating or preventing a pathology associated with an ORFX-associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Movel human polypoptides and polynoclassides useful for diagnosing, preventing and treating cardiovascular disease, neurodegenerative, hyperproliferative disorders and autoimmune disorders.
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useful for treating burns,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; SEQ ID 14626; 1037pp; English.
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66.7%; Fred. No. 87;
incisions,
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and determining the amount of bound protein in the sample. The polyreptides may be used as antipeles in the production of antibodies specific for P acres proteins. These antibodies can be used to
                                             pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis. P. acres is also involved in infections of bone, joints and the central nervous system, however it is particularly involved in the inflammatory lesions associated with acre vulyaris. A method for detecting the presence or absence of P. acres in a patient comprises contacting a sample with a binding agent that binds to the proteins of the invention
                                                                                                                                                   Sequences AAHR4105-AAH68017 represent Propionibacterium aches immunoquento polypeptides. The proteins and their associated CNA sequences are used in the treatment, prevention and diagnosis of medical conditions caused by P. aches. The disorders include SAPHO syndrome (synovitis, ache,
                                                                                                                                                                                                                                                                          Propionibacterium acnes polypeptides and nucleic acids useful for vaccinating against and diagnosing infections, especially useful treating acne vulgaris -
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02 JUN-2000, 2000US-208841P
07-JUL-2000, 2000US-216747P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SAFRO syndrome, syncytris, acno, pustulosis; hypertosis; ostoomyolitis; uveitis, endophthalmitis; kone; joint; onntrai nervous system; ELISA; inflammatory lesion; acne vulgaris, enzyme linked immunosorbont assay; dermatological; osteopathic; neuroprotectant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
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N.R. The sequence data !
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            bone degenerative disorders, or periodontal disease, and for gut protection or regeneration and treatment of lung or liver fibrosis, reperfusion injury in various tissues and conditions resulting from
                                                                                                                                                                                                                                           Example 1; SEQ ID No 17586; 1069pp; English
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Matches 4
AAU14602-AAJ14794 represent hovel bone marrow polypeptides of the invention. The proteins and corresponding moding sequences may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate bone marrow polypeptide expression. For example, to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of the polypeptides by expressing inactive proteins or to supplement the patient's own professing inactive proteins or to supplement the patient's own professing inactive proteins or to supplement the patient's own professing inactive proteins, by inserting the nucleic acids may be used to produce the polypeptides, by inserting the nucleic acids into a host cell and culturing the cell to express the protein. The nucleic acids into a host cell and culturing the cell to express the protein. The nucleic acids in the acid is DNA probes in diagnostic assays to determ and quantitae the prosence of similar nucleic acid sequences in samples, and therefore which patients
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Ren F, Drmanac RT;
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20-UTN 2000: 2000US-0598075.
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30-NCV 2000; 2000US-0250683.
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E.Eawarabayasi, Y., Sawada, M., Huikawa, H., Huikawa, I., Hin, H., Hamaman, C., Comm. M.; Ohfuku, Y.; Eunabashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, Z.; Kushida, N.; Cquoh DNA Res. 5, 55-76, 1989.
A.Wittle: Complete sequence and gene organization of the gundme of a hyper thermophilic A.Reference number: AV1000, MUID.28344137, FMID.2679194

Y., Sawada, M., Herikawa, H., Haikawa, Y., Hine, Y., Yabadanta, G., Sekins Funahashi, T., Tanaka, T., Kudoh, Y., Yamazaki, J., Kushida, N., Cquohi,

D.Kins

T;Accession: A71020

C;Genetics: A;Gene: PHI

PH1454

A, Note, this accession replaces an interim accession for a sequence replaced by GenBank

A.Tross-references - RE-Argongs, HIP gROADIS, HID BLASSE, I, FID gROADIS, A.Experimental source: strain OT3

A;Status: preliminary; nucleic acid sequence not shown; translation not shown

A; Molecule type: DNA A; Residues: 1-241 < YAW>

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R.Cole, S.T., Brösch, K., Farkhill, J., Garnier, T., Churcher, C., Harris, D., Gardan, R. Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S. Rajandream, M.A., Rogers, J., Rutter, S., Seeger, K., Skelton, S., Squares, S. Nature 393, 537-544, 1998
Nature 393, 537-544, 1998
A;Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, H.G.
A;Fitle: Deciphering the biology of My.: Anthorse subset A79500, MIII 98295087; PMIP: 429218118 for the capture of the procession: D70847
A, Status: preliminary nucleic acid sequence nut shows, translation of them.
A Molecule types hypothetical protein PH1454 - Pyromomous holikoshii C:Species: Pyrococcus horikoshii C:Date: 14-Aug-1999 #sequence_revision 14 Aug-1998 #tovt_change Colden 2008 A,Residues III21 kubb A;Oross-references GR ALG31428, GR AL1314444, NIP gRZF1514, FILM CAA14240.1; PHD:q2R08714 A;Experimental source: strain H37Rv C:Genetics: hypothetical protein Pv0059 - Mycobacterium tuberculosis (strain H7PV) C;Species: Mycobacterium tuberculosis C;Date: 17-Jul 1998 #sequence_revision 1/ Jul-1998 #text_change 20-Jun-2006 C;Accession: D70847 Ph A/Gene: RV0059 0, Superfamily Myochaoterium outerculosis hypothecical protein PV/059 A71020 A, Molecule type. DNA RESULT 2 Matches Query Match y Match 100.0%, Gothe C, TB 2, Longth 230; Loral Similarity A6 7%; Pred No. 66; thes 4, Conservative 2, Mismatches 0, Indels 26 WIVWHF 31 1 WXXWHF 6 Gurdum, S., olroyd, S.,

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RESCOVER, T.E. Elan, M.I., Erwin, A.L., Mindyachi, C.E., Werrender, E., Hickey, adman, S., Yuan, Y., Erdy, I.I., Chilter, C.H., Filger, K.F., Kas, A., Larkig, Lory, S., Cison, M.V.

Nature 400, 959-904, 2000

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A;Molecule type: DNA
A;Residues: 1-358 <STO>
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A;Gene: AGR C 1453 A;H)p p:sitT_r \sim 0.3
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A; Residues: 1:386 < KUR>
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R.Miorman, W.C.; Feidblyum, T.M.; Paulsen, I.T.; Molecn, W.R.; Firen, T.; Hendelcer, E.; Jul, M.C.; Ner, E.; C.; L. R.; S.; C.; Swith, M.L.; Bieft, D.H.; Koli, D.H.; Koli, Ermuluera, M.; Wilte, C.; Califelj, E.T.; Chafir, T.; Menter, J.C.; Franci, T. Proc. Natl. Acad. 2011. U.S.A. 98, 4136-4141, 2001.

A)Title: Complete Genome Sequence of Cautobacter crescentus.

A)Roferrance number: A87249, MUID.21173699; FMID::1259647

A)Accession: A87296
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J. Mol. Biol. 235, 472-485, 1994
E.Title. A caulthoute DWA wellylleaders that functions only in the productsional cellaration trader: 843876, MUID:04116303, EMID:8288276
E.A.Accession: 843876
E.A.Accession: 843876
A.Ascatus: preliminary
E.A.Molecule type: DNA
A.Boordanes: 1.158 27088
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A,Reference number: A97359, EMID:11743194
A,Accession: A97456
                                                                                                                                                                                                    RyGoodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurclio, B.; Gooman, A.; Elu, F.; Wellam, C.; Allinger, M.; Ewwyhry, D.; Schit, C.; Lappas, C.; Markels, F.; Crister 204, C101 C108, 2001
b.Title Genate Ledwenter of the Flant Eathers and Eletechnology Agent Agrobacterium tumm
                                                                                                                                                                                                                                                                                                                                                              Jenine specific methyltranoferase CMET (* 1850 methylase CMET) [Impore)
CySpecieu. Ng.kusterium tuneformens
CyDaner Jo sep 2001 #sequence_revision 30-3ep-2001 #text_change 17 May-2002
CyAccession: A97456
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C)Suite: lunder-lund #sequence_revision in Eugeninia #room_change 10.Sep-1999

C)Accession: $43876
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A;Cross-references: GB:AE007869; PIDN:AAK86602.1; PID:g15155772; GSPDB:GNCC169
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Died M. 13e+02;
D, Mismatched 0
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R:Wood, D.W.; Setubal, Y.C., Manl, P., Manks, D., Chen, I., W.-d, G.E.; Chen, Y.; Wad, erage, G.; Giller, W.; Grant, C.; Guentliner, D.; Eutyavin, T.; Levy, R.; Li, M.; McClel, Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon Karm, Ster, E.W.
                                                                                                                                                                                      A;Genome: nt
C;Keywords
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A;Molecule type:
A;Residues: 1-38
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A; Residues: 1-394 < DOU>
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Mature 410, 1091-1094, 2001
A;Title: The highly reduced genome of an enslaved algal nucleus
A;Reference number: Aggas; Multi-11321671; PMIT: 11321671
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A;Accession: AD2674
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C;Species: Agrobacterium tumefaciens
C;Date: il:Jan_2002 #sequence_revision il (an.2002 #text_change 17.May.2002
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                                                                                             Pred. No. 1.4e
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pred. No. 1.4e+02;
pred. No. 1.4e+02;
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Pred. No
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PTS system galactical specific enzyme IIC component homolog lin2814 [imported] (Species: Listeria innocua C;Daecies: Listeria innocua C;Date C7-Nov-0704 #sequence_revision 27 Nov-2001 #text_change 14 *Drc-2001 C;Accession: AH1783
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A/Experimental source: strain EGD-e
C)Genetics:
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R;DelVerchio, V.G.; Kapatial, V.; Redkar, R.J.; Patia, G.; Mujer, G.; Los, T.; Ivanova, I.

R;DelVerchio, V.G.; Kapatial, V.; Redkar, R.J.; Patia, G.; Mujer, G.; Los, T.; Ivanova, I.

Razur, M.; Galtsman, E.; Selkov, E., Elsei, F.H.; Hajius, G.; CrGallarbin, D.; Lotron

Proc. Natl. Acad. Sci. U.S. A. 93, 443-448; 2002

A;Title. The genome sequence of the facultative intracellular pathwhen Brucella Melitons

A;Peference number: AD1250; PMID 11756688

A;Accession: AF3432
                                                                                                                                                                                                                                                                                                                                                                     A;Molecule type: DNA
A;Residues: 1-423 <GLA>
A;Gross: Herendes: GB:
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A,Authors: Preft, T. Simmes, N., Tierrez, A., Varguez et al.

A;Title: Comparative genomics of Listeria species.

A;Reference number. AB1677, MUID 219-0274, FMID 110-73669

A;Accession AH1407

A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C.Species. Listeria monocytogenes
(Date: 27 New 2001 #sequence_revision 27 New 2001 #text_change 14 Pec 2001
(C)Accession: AH1407
(B)Glaser, F., Frangeul, L., Buchrieser, C., Amend, A., Badwetw, F., Betche, F., Dominguez-Bernal, G., Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; D.; Jones, L.M.; Karst, U.
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A/Gene: BME1444
A/Map position: I
G/Superfamily: site-specific DNA methyltransferase (adenine-specific)
G/Reywords: mathyltransferase, 3-adenise/Phathicnine
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CrDare: 01-Reb_2002 #sequence_revision 01 Reb_2002 #text_change 12 May-2002
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C;Superfamily: phosphotransforase enzyme II galactitol specific
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A; Experimental source: strain 16M
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RyGlaser, P.; Frangeul, h.; Buchieser, G.; Amend, A.; Baquero, F.; Berche, P.; Bloecker, D.; Dominguez-Bernal, G.; Euchaud, E.; Putand, L.; Pussutget, O.; Entlan, K.D.; Fsthi, H. Sciente Js., 23 and 25 toll
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C/Superfamily, usega i fatty acid decatarae
C/Keywords, oblocoplast, oxidoreductase
F/1-40/Domain, transit peptide (chineplast) #stacus prodicted
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J. Biochem. 122, 1224 1232, 1327
A.Thicle Coming of a gene for Alberghest emega 6 depatrated of a green alga, Chlamydom A/Reference namker: JC5831, MCID:98158334; PMID:9498583
A/Accession: JC5831
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C;Genetics:
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A;Threns, 27/3, 40/3, 100/3, 115/3, 222/3, 388/3
C;Superfamily, garden pea SAP DMA binding protein
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A;Residues, 1-439 <DANS
A;Crass references, EMBC.AFCCCCT1, NIF.JCISIISI, FIB.JCISIIS9, SCFCB.CNCCCC3, ATTICLT TMC
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C2Eproles: Arabidopsis Thaliana (mouse-ear cress)
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SUMMARIES

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SUBCELULIAR LOCALION: CHLOROPLAST, MEMBRANE-BOUND (PRORAPLE)
DOMAIN: THE HISTIDINE BOX FOMALIS MAY CONTAIN THE ACTIVE SIT
AND/ OR BE INVOLVED IN METAL ION BINDING.
SIMILARITY: RELONGS TO THE FATTY ACID DESATURASE FAMILY.
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FINGTION CHAPSOPHAST CMESA-6 PATTY ACTO DESATURASE INTERQUICES
THE SECOND FOURLESSALIN THE BIOSYNTHESIS OF 16.3 AUD 18.3 EARTY
ACTOS, IMPORTANT CONSTITUENTS OF PLANT MEMBRANES. IT IS THOUGHT
TO USE PERPENCIN AS AN ELECTRON DONOF AND TO ACT ON FATTY ACTOS
ESTEPHIETED TO GALACT LIPTIS, SULPOLIPTIS AND PROSCHATIFYLGLYCEPOL

OF THE CONTROL OF THE CONTROL
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181; FA_desaturase; 1.
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2; Mismatches
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Fred. Mc.
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                                                                                                                                   HISTIDINE BOX-3
                                                                                                                                                                                                      OMEGA-6 FATTY ACID DESATURASE.
                                                                                                                                                                                                                                      CHLOPOPLAST (BY SIMILARITY)
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                                                  Matches
                                                                          Query March
Best Local .
                                                                                                                                                                                                                                                                                                                                         between the Swiss institute of the first are no restrictions on its the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.lsb-sib.ch/albounce/
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MEDCINE:21016721; FireMed:11139714;
MEDCINE:21016721; FireMed:11139714;
Tabata S., Mancko T., Nakamura Y.,
Tabata S., Fancko T., Nakamura T.
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Hypothetical protein Arsg27120
ATSG27120 0g TMC21804.12 0g TC184.30.
Arsbidopsis thaliana (Mouse-ear cress).
Brkarysta; Viridiflattae; Streptoffyya; Entryophyta; Trachoophyta; Eskarysta; Viridiflattae; Streptoffyya; Entryophyta; Trachoophyta; Magnoliophyta; Postdao; Sperrarygbyta; Magnoliophyta; Postdao; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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01-NOV-1997 (Rel
15-JUN-2002 (Rel
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Mature 409.823-826(2000)
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                                                                                                                                                    Hypothetical protein SECUENCE 439 AA;
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ProDom; FD004104; Nop; 1.
                                                                                                                                                                                                                                                                                                                            entities requires a license agreement (some send an email to licensewish-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMRS ourstation
                                                                                                                                                                                                                                                                               EMBL, AFC07271; AAB61073.1; -.
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184 MEGMHE

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Best Local
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01-W0W-10095 (Se)

16-OCT-2001 (Re)

15-JUN 2002 (F-)
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F36(27)
P48627;
01-F2B-1996 (Rel. 33, Created)
01-F2B-1996 (Rel. 42, Last sequence update)
15 JUN 2010 Fel. 11, Last annituable aplate)
Comega-6 facty acid desaturase, chlorogiast precursor
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Hitz W.D., Carlung T.T., Poorb T.P.
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m. PROC487, FA debaturase, i.
Dom. PROC487, FA debaturase, i.
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32, Created)
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CMEGA-6 FATTY ACID DESATURASE
HISTICINE ECX 1.
HISTICINE ECX+7.
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RESULT 8
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                                                                                                          MEDILINE=98019091; PubMed=9358059; Kim Y.C., Miller C.D., Anderson A.J.; Wim Y.C., Miller C.D., Anderson A.J.; The major "Identification of adjacent genes encoding the major bacterioferritin from the plant-beneficial bacterium
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ProDom; PD001081; FA_desatūrase; 1.
Oxidoreduotase; Fatty anid biosynthesis; Chloroplast; Mombrane;
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30-MAY-2000 (Pel
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                                                                                                putida
                                                                                                                                                                               STRAIN-Corvallis;
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                                                                                                                                                                                                                                  NCBI TaxID-303;
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        e 199:219-224(1997).

#PINTITOR FROMMOTES HYPROJEN REFORTE IN WARTH AND OXYORN, PROTECT ORLES FROM THE TOXIC BREECTS OF HYPROJEN PEROXIDE CATALYTIC ACTIVITY & HONOLOGY - OLD) + 5 H(2)C.

**OFFACTOR: HEMB GROUP.
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L; AV04562; (AAX3979:1; L; AV04562; (AAX2979:1; ...
L; AY058078; AAL24186:1; ...
L; AY058872; AAL24240 1;
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RETTATION SMITTER
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    19, Last sequence update)
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HISTIDINE BOX-3.
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01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 41, Last anic'atirn update)
15 CTH: 2002 (Rel. 41, Last anic'atirn update)
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CHARACTERIZATION, AND MUTAGENESIS.

MEDILINE=98038777, Pubmed=9372940;
Sautier T, Relyes T, Tolleryey D, Hurr E;
Sautier T, Relyes T, Tolleryey D, Hurr E;
"Musicalar FFE(D report proteins Diffe, and Diffe interior with Topip
and are required for ribosome biogenesis.";
Mol. Cell Riol 17:7088-7997.

11- FFECTION REQUIRED FOR 612 FIR-35 MAI STRUIT STRUES II.
                                                                                                                                                                                                                                                                                                                  STRAIN-S288c / AB972;
Johnston M., Andrews S., Brinkman R., Cooper J., Ding H., Du Z., Johnston M., Andrews S., Brinkman R., Cooper J., Kirsten J., Kicaha Favello A., Fulton L., Gartung S., Greco T., Kirsten J., Kicaha Hallsworth K., Hawkins J., Hiller L., Jier M., Johnson D., Johnston L., Langston Y., Latrellle P., Mardis E., Menezes S., Johnston L., Nhan M., Pauley A., Peluso D., Rifken L., Riles L., Taich S., Trevaskis E., Vaudin M., Vignati D., Wilcox L., Wilson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STEAIN $288c / YPH1;

MEDILINE=96040178; PubMed=7547500;

MOTION F.J., Downs G. Browdgrass A.M., Gilmore T.D.;

"Genetic analysis of growth inhibition by GAI4 L Pappa P. alpha in Saccharomyces cerevisiae.";

Second Growth Differ. 6:789-798(1995).
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Proper, PD000510; CATALASE.1

PR0SITE: PS00437; CATALASE 1; 1.

PR0SITE: PS00438; PS00448; HEME LIGAND (BY SIMILAFITY).
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SIKI OP NOP56 OP YLP197W OP L8167.9.
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                                                                                                                                                                                                                                                            Submitted (SEP-1994) to the EMPL/GenPank/DDPT databases
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    -!- SIMILARITY: BELONGS TO THE CATALASE FAMILY.

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15 JUN 2002 (Rel. 41) Last amoutation update)
16 JUN 2002 (Rel. 41) Last amoutation update)
Nucleolar protein NGFS0 (Nucleolar protein NGFS),
NGFS0 CE NGFC of VERIOL (Rel.)
7 June 1977 (Veriolar (Rafvet's year))
8 Bukarylta, Elly, Av. (Veriolar (Rafvet's year))
8 Bukarylta, Elly, Av. (Veriolar (Rafvet's year))
8 Geocharomycatalor; Saccharomycoticosa; Saccharomycec,
NCB1 TaxID=4932;
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-1- SUBCRITTOR LOCATION. MAJE-31, And et al.

-1- SUBCRITTOR LOCATION. MAJE-31, And et al.

-1- SUBCRITTOR ROTTY is STRYIGHT IT is preferred through a solitary in the same of the same in t
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J. Sill. Chem. Louise463 indexiller.

M. CONOMINE EXPERIEST WIS INSIDER SENA FETTERS
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Feature E.M., Hys.ac. 7 , W.15 7 7 , Fally-resubmitted (AUG 1995) to the EMBL/GenBank/DDBJ
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This TWIDS ERTT entry is objiding It is produced through a collaboration between the Swiss Institute of Bioinformatics and the SWBG outstation the European Bioinformatics Institute the Theorem are not restrict instantials.
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ASTAGUAYS-RICH.

V.-A: RECUCES GROWTH EATS AT ALL

V.-A: RECUCES; WHEN ASSOCIATED WITH R-385.

TEMPERATURES; WHEN ASSOCIATED WITH R-385.

T >0: AT J ! (EGREE); GROWTH SLOW, AFTER TO 8 HOURS AND CELL DIVISION STOPS AFTER

20 HOURS.
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B EMBL, 275217; CAMS9630.1; -.

B EMBL, AF086770; AAC398411; -.

E COSD, COCCESS7; NOP58.

F Thirty, ITE Tran, Np.

F Ffam; PP01798; Nop; 1.

F Probom; PP06410 Nop; 1.

F Probom;
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Elady L. H., Yo M., W. X. Y., Red D. X., Char M., Char C. C., F. S.

Shar Y., End H.Y., Le G., Char M., X. X. E., Har C. S., Char G.,

Tavor, Heard C.-H., Zhou J., Hu G.-X., Gu G., Chen G. J., Chen Z.,

"Clord, and Sunctional analysis of JCDs with open reading frames

2. previously additional analysis of JCDs with open reading frames

2. previously additional analysis oxyres.cd in Just Educational Systems of JCDs and Control of JCDs with open reading frames
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0.09(XXX) 0.0900.6; 0.00EN3;

10.00T 2.001 (801. 40, Created)

10.00T 2.001 (801. 40, Last sequence update)

10.00T 2.001 (801. 41, Last indication ipdate)

10.00T 2.002 (801. 41, Last indication ipdate)

10.00T 2.002 (801. 41, Last indication ipdate)

10.00T 2.002 (801. 41, Last indication ipdate)
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CIMILAETTY BELINDO TO THE NOFO/NOFOG FAMILY.
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             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CONFLICT
                                                                                                                                                             Harron D., Gray J.O.;
Submitted (JUN-1998) to the EMPL/GenBank/DDBJ databases
--- FUNCTION- PEGUIPED BOD KOS BIRGSOMAL SUBUNIT BIGGENESIS (By
                                                                                                                                                                                                                                                                                                                                                                                                Pathus norvegicus (Bat).
Bukanyona, Mataloa; Chordara; Craniara; Vertebrata; Eufeleosromi;
Mammalia: Butheria; Podentia; Sciurognathi; Muridae; Murinae; Patrus.
NCBI_TaxID-10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16-00T-2001 (Pel 40, Last sequence update)
15-UUN-2002 (Rel 41, Last annotation update)
Nucleolar protein Nors (Nucleolar protein c
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Mel Biol cell [1:467-477/2000)
                                                                                                                                                                                                                                                                                                             MEDLINE=20143579; PubMed*10679015; Yang Y., Isaac C., Wang C., Dragon F., Pogacic V., Meier U.T.; "Conserved composition of mammalian box H/ACA and box C/D small
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16-007-2001 (Rel. 40, Created)
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15-JUN 2002 (Rel. 41, Last ann
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Ribosome biogenesis, Nuclear
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AF161469; AAF29084.1;
-2DPAGE; Q9Y2X3; HUMAN.
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MW; 27CD73CFF5B9A556 CRC64;
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01-HOV-1997 (Rel. 35, Last sequence
01-HOV-1997 (Rel. 35, Last annotati
Hypotherical 71.6 km protein TACE,
Y4CD.
                                                                                                                                                                                                                                                                             InterPro;
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                                                                                                                                                                                                                  Hypothetical protein; Plasmid. SEQUENCE 640 AA; 71600 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Molecular basis of symbiosis between Rhizoblum and legumes."; Nature 387:394-401(1997).
HE SIMILARITY: NEWE SEVICUS.
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Freiberg C A , Fellay P., Bairoch A , Broughton W J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=394;
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##BLIMF#?0135754; PubMad-10669902;

RA Amberluh G., Podlesek Z., Macek P.;

RT "A INTER DELIE in print 1 C C 1344 in taking un.

RT collagens and its putative role.";

RL Blochim. Blochys. Acta 1476:372-376(2000).

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QNNQ2; QNTXD2;

15-JUN-2002 (Rel. 41, Created)

15-JUN-2002 (Rel. 41, Last sequence update)

15-JUN-2002 (Rel. 41, Last annotation update)

16-JUN-2002 (Rel. 41, Last annotation update)

Neurotoxin Ae I precursor (Toxin Ae I) (AeNa).

Actinia equina (Buropean sea anemone).

Eukaryota; Metazoa, Chidaria, Anthoxoa; Zoantharia; Actiniaria;
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SITRAIN.Laid N., BindShaw N.;

Submitted (UTL 1996) to the EMEL/GenPank/PDP/ databasen.

-I- CATALUTIC ACTIVITY A.91 CaA + sn.gly.cetal 3 phosphatu. CaA + anyl.cetal 3 phosphatu. The salement former phosphatu.

-I- BALEMEN PHOSPHORE SUBJECTION OF MEMBERNE EIGGREETT.

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RPFO; IPRO02123; Adyltransferase;

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                                                                                                                                                                                                                                                   STRAIN.CV. COLUMBIA, Srunel D.; Fourmann M., Froger N., Brunel D.; "Amplified consensus gene markers: Tools designing for a genetic falabidusis-known-function genes in Brassica."; Submitted (JAN-2020) to the EMBL/GenBank/DDBJ databases. EMBL; AF229392; AAKONGA4 1; ...
EMBL; AF229392; AAKONGA4 1; ...
InterPro; IPR001225; FA_desatizace.
Ffan, FFITHET, FA_dusatizace, I;
FFONG; FFTHET, FA_dusatizace; I;
FFTHET, FA_dusatizace; I;
FFTHET, FA_dusatizace; I;
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Bukary '', Vittlijlich', Stimp (ply) a Embry plyta, Tritche plyta,
Sperman (plyta, Yaphiliphy), Addiniyledine, Stevelden, Suddide,
euroside (I) Brassinales, Brassinaneae, Arabidopsis.

NOBI_TartD=1700.
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Romo saptens (Human)
Fukaryota, Matacca, Chordata,
Mathaila, Eutheria, Frinates,
NCDI_Taxil.24605,
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01-DEC-2001 (TEMPRIFOL 19, Last sequence of
01-DEC-2001 (TEMPRIFOL 19, Last annotation
CDNA FLUSTERS (fix plene NTLKLUSING)
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(TrembLrel. 17, Last dimetation
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                                                                                              Conservative
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RESULT 4
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The Mark CV, K500;

Reservation H., Frieger N., Brunel D.;

The philiped consensus general markets. Tools designing for a general field consensus years in Example Ca.";

The Arabidates Market Finition general in Example Total databases.

School 10.3 ("Mi Conn. Fr. The Exph.GenDank/PCPT databases.

Explain ARZ23330; ARK00652.1;

Reservation ARZ23330; ARK00652.1;

Problem, PRO0487; FA desaturase; 1.
                    Query Match
Matches
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JEG FERENE
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SELTENTE
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Froger N., Brunel D.;
Fourmann M., Froger N., Brunel D.;
Fourmann M., Froger N., Brunel D.;
"Amplified concensus gene markers: Tools designing for a genetic
of Arabidopols known function gened in Brassida.";

Libritud Const. Const. Const. Const. Const. databases.

EMML, ARZESTERS, CARROSENIA, Const. Con
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Brassica campustris (Field mustard).
Budarycta, Trialistator, Otter phyra, Edbrychlyta, Trachesphyta,
Grenatuhyta, Majoulistyli, vodi ctylod us, otto eddicato, Rocidae,
gurocido II) Brassicales; Praesiconeso; Brassica.
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01.-HW-2001 (TrEMBLrel. 17, Last sequence update)
01.-JUN-2001 (TrEMBLrel 17, Last sequence update)
11.-JUN-2001 (TrEMPLrel 19, Line armoticion update)
0mega 6 reductase (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Reasoica napus (Pape).
Bukaryidta, Mikidiglantae, Chroptoghyla, Embryophyta, Trocheophyta;
Spermatophyta; Maghaliophyta; eudinoryledons; core eudicots; Posidam;
eurosida II; Brasaloalas; Brasaloaceae, Brasaloa.
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EADCoeff 2.
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                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A
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4; Conservative
                           Cimilarity
                                                                                          213
.14 AA;
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     Conservative
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                                                                                                  MW.
                 100.0%;
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Pred. No. 1.7e
2; Mismatches
                         Pred. No.
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                                                                                                  THE ERAFFERNDBUCOS CRC64;
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     Mismatches
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1.7e+02;
                                                  DB 10;
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RESULT 7
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Q9AXY2;
                                                                         Yamada W. Liu S. Sakano H. Pham P. W. Ranh J. Ching M. W. Goldsmith A. D. Loo J. M. Quach H. L. Tang C. Toriumi M. Yu G. Rowser I. Carminci P., Chen H. Cheuk R., Hayashizaki Y., Ishida J. Jones T., Kamiya A., Karlin-Noumann G., Kawai J., Fim C., Kossema E. Lam R. Lin J. Meyers M. Miranda M., Marisaka M., Njuyon M., Palm C. J., Sakurai T., Sarou M., Seki M., Marisaka M., Njuyon M., Shinn P. S. Southwick A., Shinnozaki K., Davis R.W., Ecker J.R., Thoologis A., Southwick A., "Full Length CDNA of Gene KIGHT 11/ATE924400 (GI:1017701)"; Submit-od (ADF 2001) Fore KIGHT 11/ATE924400 (GI:1017701) "; SUMILAPITY: CONTAINS 1 WD PEPEAT (TPP-ASP DOMAIN)
                                                                                                                                                                                                                                                                                                                                                              094K47,
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JHN 2002 (TrEMBLrel. 21, Last annotation update)
Putative 6-phosphoglucomolactomase.
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Fourmann M., Froger N., Brunel D.;
Fourmann M., Froger N., Brunel D.;
"Amplified consonsus gone markers: Tools designing for a genetic of Arabidogesis-known-function genes is Reassista.";
Submitted (JAN-2000) for the FMBL/GenBank/DPH databases.
EMBL; AF200491; AAF00664 1;
InterPro; IPR001255; FA desaturase.
                                                                                                                                                                                                                                                                                                                     Arabidopsis thaliana (Mouse-ear cress).
Eukaryora, Viridiplantae, Stroptophyta, Embryophyta, Tracheophyta,
Spermarophyra: Magnoliophyta, endicoryledops, onro endicars, Posidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Brassica napus (Rape).
Fukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta;
Spermatophyta: Magnoliophyta: sudicotyledons, core sudicits, Rusiduu;
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMPLrel. 21, Last annotation update)
                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
Yamada K., Lin S.X
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                                SEQUENCE
                                               TIGRFAMS; TIGR01198; pgl; 1. Pepeat; WD repeat.
                                                                                                                                                                                                                                                                                                         eurosids II; Brassicales; Brassicaceae; Arabidopsis
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216 AA,
                                  repeat.
219 AA;
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216 MW,
                                24542 MW;
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                                1994A723D2434B8A CRCC4
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PB 10;
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Length 219;
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RESULT 9
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MEDLIME-19205987; PubMed-9634230;
Gold S.T., Brosch R., Parkill J., Gainard T., Churcher C., Harris D.,
Gordon S.V., Eigherier K., Gas S., Barry C.E. III, Tekaia F.,
Eadron R., Fusham D., Promit J., Lillingwith T., Timer R.,
Bavies R., Devlin K., Feltwell T., Gentles S., Hamish M., Helynyd S.,
Hornsty T., Jagels Y., Yrogh A., McLean J., Monle S., Murphy L.,
Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
Parter S., Seeger K., Skelton S., Squares S., Squares R.,
Sultter J., Eagler K., Whitehead S., Barroll B.G.,
"Deciphering the biology of Mycobacterium tuberculesis from the
complete genome sequence.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01 JUN-1998 (TrEMBLrel. 06, Created)
01.JUN-1998 (TrEMBLrel. 06, Last sequence update)
01.MAF 2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical protein Rv0059.
RV0059 OR MTV030 02 OR MT0065.
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Q9AXY4,
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Pfam; PF0497, PA desaturase, 1.
ProDom; PD001081; PA desaturase; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fourmann M., Froger N., Brunel D.;
"Amplified consensus yene markers. Tools designing for a genetic map
of Arabidopsis-known-function genes in Brassica.";
submirred (ANN 2000) to the EMWL/SenMank/DDPZ ditabases.

EMBL, AFCCORRS, AAKCOKKI 1;
InterPos, IPPOSIZES, FA decaturase.
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01-JUN-2001 (TrEMBLrel. 17, Last seguence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
00093a_6_reductase (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mycobacterium tuberculosis.
Banteria, Firminutes; Antinobacteria, Antinobacterida
Antinomynetales, Corynebacterindae, Mycobacteriadeae,
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Hadamooto S., Sekhe M., Eaka S. I., Kostoji H., Holbawa K.,
Isakai M., Saka H., Holbawa H., Takataya M.,
Fundhauli T., Tanaka T., Kadali Y., Hadauki C., Kuchida H., Spothi A.,
Aoki K. Y., Siliaya H., Kikada H., Hadauki C., Kuchida H., Spothi A.,
Maccalli Y., Elizaya H., Kikada H., Fitt F.T., Hirli E.,
Holbawa T., Kadali Y., Fitt F.T., Hirli E.,
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MINIMAL JERGITT, LLEMNAH POCCETT;

FIRED TW., Dirling T., WHILLE D., OLITIN G.G.,

Cleve F., Swinz M., Hiskey E.K., Clayton E., Ketchum K.A.,

Cleve F., Swinz M., Hiskey E.K., Clayton E., Ketchum K.A.,

Clayton E., Hardland T.M., Mote J.M., D., Libberg S., Peterson J.,

Finalak H., Stokadsen T., Howell T. M. F., Claytan Aryan M., Unterphask T.,

MINIMAL E., Hotel K., Bebeits K., Sandunky M., Weldman J., Smith H.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         08250; CHEMBEROL 08, Created)
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01-NOV-1998 (TrEMBEROL 08, Cast seguence update)
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InterPro; IPFGGG561; EGF-like.
InterPro; IPFGGG561; EGF-like.
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Pfam; PFGD557; VanY; I.
PKUSIIK; PFGGGG27; EGF I; GNKNONN_I.
Carboxyperidado; Completo proteome.
SEGULENCE 250 AA; 20103 MM; PEDFGID45133FFR6 CEC64;
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Easteria, Spirsola,
NCBI_TaxID-160;
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d-plosphograduchauterase like protein.
Arabid-pade thaliana (Nouse despringer)
Elkaryota, Viriliplantase, Otteptophyta, Elksysphyta, Trackeophyta;
Spetraliplantase, Highland, Otteptophyta, School, Otte usdiction, Rosid
spetraliplantase, Mighland, Franchisadosae, Arabidepsis.
                                                                                                                                                                                                                                                       Venter J.C.,
"Cimplete genera sequence of Traporoma pillidum,
spirochete",
Science 281:375-388(1998).
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TP0221.
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RX Galadan U.E. Nighaum C. Pry A. Endrizzi M.G. Macdruid P.

RA Galadan U.E. Nighaum C. Pry A. Endrizzi M.G. Macdruid P.

RA FitzHugh W., Calvo S., Engels P. Smirnov S., Armore D., Prown A.

RA Allen N., Maylor J. Orange-Th-main. N., Pakiellade F., Chinson P.

RA Almon L., McEwan P., McKernan K., Talamas J., Tirrell A., Yo W.

RA Zinmer A., Barber R.D., Cann I., Graham D.E., Grahame D.A., Guss A.M.

RA Zinmer A., Barber R.D., Cann I., Graham D.E., Grahame D.A., Guss A.M.

RA Zinmer A., Li W., Liu J., Nichopathyny B., Feeve J.M., Smith E.,

PA Springor T.A., Theyam L.A., White O., White P. H., Je Majari' E.G.,

RA Pritchett M., Sowers K.P., Swanson R.V., Zindor S.H., Lander E.,

RRA Pritchett M., Sowers K.P., Swanson R.V., Zindor S.H., Lander E.,

RRA Metcalf W.W., Birren B.;

"The genome of Methanosarcina anotivorans reveals extensive metabolic and physiological diversity";

Lander R.T.

"The genome of Methanosarcina anotivorans reveals extensive metabolic and physiological diversity";
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SEQUENCE FROM N.A.

STRAIN-ATCC 15692 / FAO1;

MEDLINE=20437337; PubMed:10984043;

MEDLINE=20437337; PubMed:10984043;

Stover C.K., Pham X.-Q T., Erwin A.L., Mizoguchi S.D., Warrener P. Garber R.L., Goltry I., Toloptino E., Westbock-Wadman S., Yuan Y. Garber R.L., Coulter S.N., Friger K.R., Kas A., Larbig K., Lim R.M. Brody L.L., Coulter S.N., Friger K.R., Kas A., Larbig K., Lim R.M. Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., Reizer J., Saier M.H., Hancock P.E.W., Lory S., Olson M.V., "Complete genome sequences of Pseudominas aeruginosa PAO1, an opportunistic pathogen.";

Nature 406:959-964(2000).
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01-JUN-2002 (TrEMBLrel.
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                                                                                                                                                                                                                                    NCBI_TaxID=287;
                                                                                                                                                                                                                                                                    Bacteria, Protecharteria; gamma subdivision; Pseudomonadaceae;
                                                                                                                                                                                                                                                                                           Pseudomonas aeruginosa.
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SEQUENCE 293 AA, 32016 MW; V6A410V6EUF60DE1 CPC64;
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_PF03611; EIIC GAT, 1.
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| Peptides binding to the DRA Finding durate of transcription factor EDF and inhibiting cell cycle progression, useful for the treatment of cancer | WPI; 2000 532806/48. | Mueller R, Kontermann RE, Montigiani S; | (PPOL-) PPOLIFIX LTD. | 26-JAN-1999; 99GB-0001710. | 25 - 382 0000; 10000W0: 08002007 | | | WQ200044771-A1. | Synthetic. | psoriasis; restenosis. | transcription; apoptosis; proli | | Peprile which binds to transcription factor ESF 1 SWA binding domain. | | ON-NOW COOK (First patry) | AAB01492; | Mibolian Standard; peptide; o AA. | | RESULT 1 | |

ALIGNMENTS

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                                        Peptides which bind to the DNA binding domain of transcription factor E2F and inhibit cell cycle progression may be useful as research agents to investigate the interaction between EDF and DP-1 or the authority of transcription by EET 10F lluctualExert They may all the sould for inducing applicate and/in well cycle arrupt in a cell, particularly for treatment of causer or other proliferative and cell, particularly for treatment of causer or other proliferative
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                                                    WARWHE
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                                                                                                                                                                                                                                                                               Fage 26; 42pp; English
                                                                                                                                                                                                                                                                                                                                                             532406/48
                                                                                                                                                      6 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                2000WR GB06227.
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                                                                                                      TREETERS TO SE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    binds to
                                                                                                                                                                                                                                                                                                                                                                                                                                     3338 0001710
                                                                                                            transcription factor E2F-1 DNA binding
                                                                                                  19%; Score 6; DB 21;
7%; Fied. No. 7.8e+05;
C; Milmithy.
                                                                                                                                                                                                                                                                                                                                                                                      Montigiani S;
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RESULT 5
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    04-FEB-2000; 2000US-0180312.

26-MAY 2000; 2000US-0608496

30-JUN-2000; 2000US-0608498

03-AUG-2000; 2000US-0612366

21 SEP 2000; 2000US-0234687,

27 SEP 2000; 2000US-0236359.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Peptides which bind to the DNA binding domain of transcription factor E2F and inhibit cell cycle progression may be useful as research agents to investigate the interaction between E2F and DP-1, or the activation of transcription by E2F-1/EP-1 heterodimers. They may also be used for inducing apoptosis and/or cell cycle arrest in a cell, particularly for treatment of cancer or other proliferative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA binding, transcription factor, EDF, EDF-1, cell cycle, DP-1; activation; transcription; apoptocis; proliferative disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Peptides binding to the DNA binding domain of transcription factor and inhibiting cell cycle progression, useful for the treatment of
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                                                                                                                                                     30-JAN-2001; 2001WO-USO0669
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                                                                                                                                                                                                                                          W0200187277-A2
                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                     Human; fortal liver: gose expression, single exam mudeic acid probe
                                                                                                                                                                                                                                                                                                                                                             Peptide #8399 encoded by human foetal liver single exon probe
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Best Local
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26-MAY-2009, 2000US:0207456.
30-JUN-2000, 2000US:0632366.
03-AUG-2009, 2000US:0632366.
21-SEE-2000, 2000US:0234687.
27-SEE-2000, 2000US:0234689.
04-0CT-2000, 2000US:0236559.
                                                                                                                          Penn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human brain expressed single exon probe encoded protein SEQ ID NO: 33858.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                        Single exon nucleic acid probes for analyzing gene expression in human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    W0200157275 A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; brain expressed exon; gene expression analysis; probe;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Note: The sequence data for this patent did not form part of the grinted specification, but was obtained in electronic final line
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a peride encoded by a single exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from huma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-483447/52
                                                                                  WFI; 2001 483446/52
                                                                                                                                                                       (MOLE-)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       epilepsy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           microarray; Alzheimer's disease; multiple sclerosis; schizophrenia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAM61753 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         from WIPO at ftp wipo int/pub/published_prt_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          nucleic acid probe of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 27, SEQ ID NO 33528, 639pp + sequence listing, English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (MOLE:) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              04-00T-2000; 2000GB-0004263.
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                                                                                                                                                                    MOLECULAR DYNAMICS INC
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26 MAY-2000; 200008-0207495
30 JCN 2000; 200008-0632366
2 MAG-2000; 200008-0632366
2 MGS-2000; 200008-0632366
2 MGS-2000; 200008-0632468
2 MGS-2000; 200008-0024264
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                                                                                  The present invention provides a number of single executive and decide probability and derived from journal requestes expressed in the human brown marrow. They may be pasted for respect exercisin in blue marrow samples, which may emble the improved diagnosis and treatment of announces such as lymphoma, lenkapmia and myeloma. The present sequence is a protein encoded by one of the probes of the invention
                                                                                                                                                                                                                         Human genome-derived ringle whom such is acid grobbs weight for analysing generally solution in human k to m_{\rm eff} \times \kappa
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                                                            Sequence
                                                                                                                                                                                             Example 4; SEQ ID NO: 34855; 658pp+8equence Listing; English
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                                                            36 AA;
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   Conservative
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(6. 38)
              Chen W,
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; Score 6; UB 22; Length 36; Field, W., 25; O; Indels
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PECULT 3

AATTI4683 Standard; Protein; 43

Movel bone marrow polypeptide #82

AAU14683; 24-001-2001

(first entry)

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RESULT 8
AAM34663
ID AAM3
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30-73W 2001 200008-053256.
03-A00-20000 20008-053256.
21-SEP 1990 1000008-00236359.
04-007-2000) 200008-0024263.
                                                                                                                                                      The product invention teleton coingle each militarial probe. (SENP) one Addition ANALYSES. The present appeared to a feature follows are useful for producing a minimarity for producing, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for ordered all dispussis of human grants displayed.
                                                                                                                 Sequence
                                                                                                                                             from human placents. The
human genetic disorders.
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genetic disorder.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        04 FEB 2000;
                                                                                                                                                                                                                                                                                analyzing gene expression in human placenta -
19 WRAWHF 24
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                  1 WXXWHP 6
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                                                                                                                                                                                                                                                                                            genome derived single exem nucleic acid probes useful
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                                                                                                                                                                                                                                                                                                                                                       Hanzel
                                                                                                                 36 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               probes in diagnostic assays to detect and quantitate the presence of similar nucleic acid sequences in samples, and therefore which patients may be in need of restorative therapy. The proteins apriled in the production of antibodies against bone marrow proteins and in assays to identify modulators of their expression and accivity. The anti-hone marrow protein antibodies and antagonist may also be used.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       or deletions in a patient's genome that affect the activity of the polypeptides by expressing inactive proteins or to supplement the polypeptide. Additionally, the nucleic acids may be used to produce the polypeptide. Additionally, the nucleic acids may be used to produce the polypeptides, by inserting the nucleic acids into a host cell and culturing the cell to express the protein. The nucleic acids into a cid and its complementary seguences may also be used as PNA probes in a diagraph of the complementary seguences may also be used as PNA probes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAU14602-AAU14794 represent novel bone marrow polypeptides of the invention. The proteins and corresponding coding sequences may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate bone marrow polypeptide expression. For example, to treat disorders associated with decreased expression by recrifying mutations
                                                                                                                                                                                                                                                                                                                                                                          as diagnostic agents for detecting the presence of the protein in samples (e.g. by enzyme linked immunosorbant assay (FLISA)). The proteins may be used to regulate haematopoiesis activity, and consequently in the treatment of myeloid or lymph cell disorders; in tissue regeneration, of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              03-FEB-2000; 2000US-0496914.
20-JUN 2000; 2000US-0598075.
19-JUU-2000; 2000US-0520325.
30-NOW 2000; 2000US-0200683
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pone marrow; diagnostic; therapeutic; gene therapy; antigenic; haematopoiesis; myeloid; lymph cell disorder; tissue regeneration; wound healing; nutritional supplement; immune disorder; severe combined immunodeficiency; SCID.
ABG64892;
                                    ABG64892 standard; Protein; 53 AA
                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                        such as wound healing; as a nutritional supplement; and in treatment of immune disorders such as severe combined immunedationers (SCID).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 10; Page 248; 392pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleic acids encoding home marrow polypeptides, useful in diagnostic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     05-FEB-2001; 2001WO-HS03782
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                                                                                                                                                                             1 WXXWHF 6
                                                                                                                                                                                                                                       ocal Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                down regulate expression and activity. The antibodies may also be used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2001-488875/53
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                                                                                                                                                                                                                                                                                                      43 AA,
                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                       100.0%;
                                                                                                                                                                                                                                       Score 6;
Pred. No.
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                                                                                                                                                                                                                                                           DB 22;
                                                                                                                                                                                                                                                           Length 43;
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DEX TXX ID
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                                                                                                                                  RESULT 11
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                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                  The present invention relates to albumin fusion proteins comprising a therapeutic protein X and human albumin (HA, also known as human serum albumin, HSA). The proteins are useful for treating a disease or disorder that may be modulated by therapeutic protein X. The albumin extends the shelf life of protein X, and may increase its biological in vitro/in vivo activity. The protein is useful for treating and diagnosing disorders such as cancer, reproductive disorders, dispective disorders (e.g. grown's disease, ulcerative colitis), immune disorders (e.g. armired immunedafiliency syndrome, AITS), endorine disorders (e.g. diabetes), haematopoletic disorders, neural disorders (e.g. diabetes), haematopoletic disorders, neural disorders (c.g. Alzheimer's, Parkingon's, Creutzfeldt Jacob disease, encephalomyplitis, meningitis, schizephrenia), and connective disorders (e.g. esterporesis, arthritis).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           digestive disorder; immune disorder; endocrine disorder; hasmatopoietic disorder; neural disorder; connective disorders; antiinflammatory; antiulcer;
                                 01-JUL-2002
                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12 AFR 2000; 2000US-229358P
25 AFP 2000; 2000US-199384P
21-DEC 2000; 2000US-256931P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          neuroprofective; antiparkinsonian; antimicrobial; neuroleptic; osteopathic; antiarthritic.
                                                                 AAE21233;
                                                                                                   AAE21233 standard; Protein; 53 AA
                                                                                                                                                                                                                                                                                                                                                         fusion proteins of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Page 1582; 2102pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 albumin fused to a therapeutic protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New fusion protein for treating disease e.g. diabetes comprises
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rosen CA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12-AFR-2001; 2001WO-US11988
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human albumin fusion protein #1567.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27 - AUG - 2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            human serum albumin; HSA; cancer; reproductive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            immunomodulator; anti-HTV; antidiabetic; harmogratic; nootropic;
                                                                                                                                                                                   21 WASWHF 26
                                                                                                                                                                                                                     1 WXXWHF 6
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                                                                                                                                                                                                                                                     4; Conservative
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                                                                                                                                                                                                                                                                                                                       53 AA;
                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein; therapeutic protein X; human albumin; HA
                                                                                                                                                                                                                                                                     100.0%, Score 6, DB
66.7%; Pred No 35;
                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                  , cc ac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  disorder;
                                                                                                                                                                                                                                                                                     Length 53;
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Human gene 18 encoded secreted protein HNNBM45,

SEQ

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Human, secreted protein; immune disorder, antiallergic, antixheumatic, theumatoid archritis; breast neoplasia; breast cancer; antiarchritis; neurological disoace; Althoimer's disoace; Parkinson's disoace; trauma; murchite cyldiche, elugidalis, cyldiali, kachistati, anderia, coli, antiinfancatory, philadealcylcal, dermatolydial, lenuncetheulativ, mini, antinomedial cyldial dermatolydial, lenuncetheulativ, gene therapy, autoimmune disoace; Bentington's disease; moningitis, demystiating disease; peripheral neuropathy, congenital malformation; spinal cirdicity, poripheral neuropathy, congenital melformation; spinal cirdicity, poripheral neuropathy, schaemia, perception, miniple ecleosis, infarction; baemorrhage; schizophrenna, dementia; depression, panic disorder, learning disokility, ALS, feeding disorder, peripheral indicator, learning disokility, ALS, feeding disorder, constant in disorder, learning disokility, ALS, feeding disorder, constant disorder, learning disokility, ALS, feeding disorder, constant disorder, behavioural disorder.
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Homo sapiens.

Rey Location/Qualifiers
1.31
2.32
2.53
2.53
2.54
Atture_secreted_protein
Mis. difference 55
Anthrop 71
Anthrop 72
Anthrop

W0200216390-A1

28-FEB-2002.

17-JAM-2001; 2001WO-US01435.

13 -AUG-2000; 2000US ALEASE

(HUMA-) HUMAN GENOME SCI INC

Rosen CA, Elmathird W., Faket H., Eitse le, Eighet Le, Elsed HD, Moore PA, Wei P, Ebner P, Dwan DP, Shi Y, Choi GH, Fiscella M; Ni J,

WPI; 2002-304113/34 N-ESDB; AAD33734.

An isolated nother acid molecule (1) comprising a polynocleotide which encodes a polynoptide useful in the diagnosis and treatment of disorders e.g. immune disorders -

Claim 11, Page 504, C34pp, English.

AAD31692-AAD33716 represent cDNAs corresponding to 21 human secreted CC AAEC1235 AAEC1235 represent the proteins they encode CC AAEC1235 AAEC1235 represent the proteins they encode CC AAEC1235 AAEC1235 AAEC1235 represent the proteins they encode CC AAEC1235 AAEC1235 AAEC1235 AAEC1236 AAEC12

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AAU66178
ID AAU6
Query Match
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11 122 1111,
07 177, 2000;
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b'maisonneuve J, Zhang Y,
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dermatelegical; osteopathie; neuroprotectant.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Supjunitablesium admic polypoptided and baddeid adde deeful fo valctinating against and diagnosing infections, especially useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     W::, 2001 815774/71.
N-PSDB; AASS9718.
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uveltis, endephthalmitis, bose, joint, mentral mermous cyctem,
httlumnuttry lector, ache pulgarie, endyse liched lemanosorbent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Propionihasterium asses immunsyenis protein #27074
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1981 - Alimin III.
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2000US 216747P
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, Jen S, Carter D;
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2, Mismatches
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RESULT 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; open reading frame; ORFX; gene therapy; cancer; cirrhosis; hyperproliferative disorder; psoriasis; benign tumour, haemorrhage, degenerative disorder; osteoarthritis; neurodegenerative disorder; osteoarthritis; neurodegenerative disorder; cardi-vastular disease; disease; immune deficiency; immune disorder; infectious disease; autoimmune disorder; rhormatoid arthritis, autoimmune thyrillitis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel buman polypoptides and polymorlessides useful for diagnosing preventing and treating cardiovascular disease, neurodegenerative, hyperprolliferative disorders and autoimmune disorders
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                     diseases, autoimmune disorders such as multiple sclerosis, rheumatoid arthritis, autoimmune thyroiditis, myasthenia gravis, graft-versus-host disease and autoimmune inflammatory eye disease open proteins are also
                                                                                                                                                                                       treatment of cancer, hyperproliferative disorders, cirrhosis of liver, psoriasis, benign tumours, keloid, degenerative disorders, haemorrhage, osteoarthritis, neurodegenerative disorders, disorders related to organ transplantation. cardiovascular diseases, diabetes mellitus, systemic
                                                                                                                                                                                                                                                                                                                                treating or preventing a pathology associated with an ORFX-associated disorder in humans, and in the manufacture of a medicament for treating syndrome associated with OPFX-associated disorder OPFX Phylmologotide sequences can be used in denotification of the contraction of the c
                                                                                                                                                                                                                                                                                                                                                                                                                                                               (referred to as open reading frame, ORFX, where X is 1-11491 (see
in the specification). APM15762 to ARM27252 encode the human ORFX
proteins given in ABP00010 to ARP11500. ORFX proteins are useful
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useful for treating burns, incisions,
                                                                                                                       lupus erythematosus, hyportension, hypothyroidism, choleste storage disease, various immune deficiencies and disorders,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; SEQ ID 14626; 1037pp; English.
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29-AUG-2000; 2000US-228716P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  present invention describes substantially purified human proteins ferred to as open reading frame, ORFX, where X is 1-11491 (see Table 1) the coordination APMISTS to APMISTSS encode the human ORFX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2002
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66.7%, Pred. No. 37,
Fivo 2, Migmatches
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pustulosis, hypertosis and estromyciltis) uveitis and endophthalmitis. P acres is also involved in infections of bone, joints and the central nervous system, however it is particularly involved in the inflammatory lesions associated with acre vulgaris. A method for detecting the presence or absence of P, acres in a patient comprises contacting a sample with a binding agent that binds to the proteins of the invention and determining the amount of bound protein in the sample. The polypeptides may be used as antigens in the production of antibodies specific for P, acres proteins. These antibodies can be used to
                                                                                                                                                                                                                                                                                                                                                                                             Skeiky YAW, Persing DH, M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NATHO syndrome, synewitis, acme, pustuledis, lypertholic, etwimouveitis; endophthalmitis; bone; joint; central nervous system; linflammatory lesion, acme wilgaris, enzyme linked immineerthop; dermatological; osteopathic; neuroprotectant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       home degenerative disorders, or periodontal disease, and for gut protection or regeneration and treatment of lung or liver fibrosis, reperfusion injury in various tissues and conditions resulting from
                                                                                                                                                       polypeptides. The proteins and their associated DNA sequences are used the treatment, prevention and diagnosis of medical conditions could be also as the disorders include SAPHO syndrome (synovitis, acne,
                                                                                                                                                                                                       Sequences AAH39105-AAH68017 represent Propionibacterium acmes immunogenic
                                                                                                                                                                                                                                                                                           Propionibacterium aches polypeptides and nucleic acids useful for vaccinating against and diagnosing infections, especially useful
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2000; 2000US 216747P
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ANTIAGO ANTIAGO represent novel becoming colling sequences may be used in the prevention. Alagonais and corresponding colling sequences may be used in the prevention, diagonais and therefore diseases associated with inappropriate beneficiated with dorroased expression. For example, to treat discrete secritated with dorroased expression by restifying mutations or deletions in a parison of gonome that affect the outlity of the polymerists by expressing inactive gonome that affect the outlity of the polymerists by expressing inactive gonome. And thought the nucleic acids may be used to professing inactive gonome. And thought the nucleic acids may be used to profess the polymerists, by inserting the nucleic acids into a host of its profess the polymerists, by inserting the nucleic acids into a diagnostic assays to detect and quantitate the presence of similar nucleic acid assays to detect and quantitate the presence of similar nucleic acid segmences in samples, and therefore which patients
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bone marrow; diagnostic; therapeutic; gene therapy; antigenic; baena opolesis; myeloid; lymph cell disorder; tissue regenerat would healing; nutritional supplement; inmune disorder;
                                                                                                                                                                                                                                                                                              Claim 10; Fage 137; 392pp; English
                                                                                                                                                                                                                                                                                                                                                          Nucleic acids encoding bone marrow polypeptides, useful in
                                                                                                                                                                                                                                                                                                                                                                                                                           WPI;
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Ren F, Drmanac RT;
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20-UUN-2000, 2000US-0598075.
19-UUN-2000, 2000US-0520325.
30-NeV-2000, 2000US-0250683.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel bone marrow polypeptide #176.
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67 WLIWHF 72

Job time : Search

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NIBS2/37374** AJORDSON; Jennesemp.combl/AA1940 DAT**

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SIRS2/3734** AJORDSON; Jennesemp.combl/AA1940 DAT**

KIRS2/3734** AJORDSON; Jennesemp.combl/AA1940 DAT**
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Pred. Not is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution

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| AAU75412 | AATTT 5.2.2.3 | AA1179154 | AAE20851 | ABG63324 | AAU99514 | AAE12406 | AAE13132 | NAME 2570 | AAE13402 | ARR79000 | ABGDREDT | ABG04111 | MAU70773 | MAC00040 | AAU90618 | AAB76904 | AABneles | MAE19239 | AAUR6045 | AAU77026 | AVAEEUR | AAY30381 | AAE07760 | ABF46201 | NAW38112 | AAY88154 | | AAR57401 | AAB20714 | AAW62149 | AAR57400 | WALLSOLD | AAB01498 | AAR57399 |
| Throug decrosis | Consensus signal | Cynthetic consen | .3 | Eynthetic signal | 173 | Consensus signal | Consencus signal | Consensus signal | Constitute sigani | 2 | . Brima | l human | Hepatitic B virus | ilih/insulin | Insulin/insulin- | 0 ×2111 | Heparitis GR virus | 17 | receptor receptor | 1 | Oestrogen receptor | pe de | T VTH | Human BLyS binding | Dystrophin WW doma | Oregon green 514 | green | f or | 3 | ophilus | Peptide for trea | 7 | w) i i | Peptide for treati |

ALIGNMENTS

| RESULT 1 AAR57386 ID AAR57386; XX AAR57386; XX 21-MAP-1995 (first entry) XX XX XX Poptide for treating dispases related to anti-DNA antibodies. XX XX YW Carrier, absorbing agent, 'reathment, anti-DNA antibodies. XX YM PO6192290-A. XX XX YP06192290-A. XX XX PP0 12-UU,-1994. XX PP RR 30 SEC 1992, 92UF 0261821. XX XX PP PR XX XX XX PP A peptide and an adsorbing agent from the investigated to anti-DNA PP A peptide and an adsorbing agent from the investigated to anti-DNA PP PR A peptide and an adsorbing agent from the investigated to anti-DNA PP PR A peptide and an adsorbing agent from the investigated to anti-DNA PP PR B positions and immune complexes XX Disclosure, Page 11, 14pp, Japanese. CC The sequences given in AAR57386 413 are peptides which are all covered |
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                                          n = 2-5.
These peptides may be immobilised on a carrier in taborbing agent which may be used in the treatment to anti-DNA antibudies unl/in immore timpos.
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H X (A B)n T Z

A = Trp, Phe or a peptide fragment consisting of 2 residues;

B = Trp, Phe, Asn or Glu;

X and Y - a bond or Asp Clu, Arg, Lyc, Hic or a poptide fragment consisting of 2-10 residues, provided that at least one X or Y are present;

Z = CH or NH2; and
                                                                                                                                                                                                                                                                       A poptide and an admirthing agent graph by carrier useful for treatment of diseases
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                       Sequence
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                                                                                                                                                                                            The sequences given in ARFIDER 41% are \{\psi_{I}^{(i)}\}\} by the claimed generic formula:
                                                                                                                                                                                                                                  Disciosore: Page 11: 14pp: Japanese
                                                                                                                                                                                                                                                           antibodies and immune complexes
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B - Trp,
B and Y
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                                                                                       = CH or NH2; and = 2-5.
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                                                                                                             Phe or a peptide fragment consisting of 2 residues;
Phe, Ash or Glu;
A bond or Acp. Glu, Arg. Lys, Hid or a peptide fragment
consisting of 2 10 residues, provided that at least one
X or Y are present;
X or Y are present;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             absorting
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Mutches 3, Conservative
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Peptide which binds to transcription factor E2F 1 DNA binding domain
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100.0%,
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Pred. Mo. 7.8e+05;
2, Milmaille. 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PMA binding: transcription factor, E2E, E2E 1, cell cycle; DP-1, activation; transcription, apoptosis, proliferative disorder,
                                                                                    DMA binding, transcription; factor, EDP, EDP 1, cell cycle, DF activation; transcription; apoptosis; proliferative disorder; psorlasis; restenosis.
                                                                                                                                                                                                                                                                                                                                                                                 Sequence
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Misc-difference
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Best Local
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                                  WFI, 2000 522806/48
                                                                                                           26-JAN-1999;
                                                                                                                                                                                                                                psoriasis; restenosis
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                                                          Mueller R,
                                                                                  (PROL-) PROLIFIX LTD
                                                                                                                              26 JAN 2000; 2000WO-GB00227.
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                                                                                                                                                                                                                                           activation; transcription;
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Local Similarity 83 3%; Pred No 7 80+05;
Les 5, Conservative 1, Mismatches 5,
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apoptosis; proliferative disorder;
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                                                                                                                                                           peptides which bind to the NWA binding domain of transcription force property and inhibit cell cycle progression may be deserted as presents agents to investigate the interaction between EDF and DP-1, in the filterior for the control of EDF (TDF inhibition) and They may also be used for inducing approxis and/or cell cycle arrest in a cell, particularly for treatment of concer or other proliferative disorders such as psoriasis and restenosis.
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       対 5 次 号 次 号 交 登 度 度
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Peptidus which bind to the DNA binding domain of transcription factor B2F and inhibit cell cycle progression may be useful as research against to investigate the interaction between B2F and DP-1, in the autivation of transcription by ECF 1/DP 1 beneficiation. They yet activated for including the binder of the cycle acrest in a cell galactic by 51 telephone for their principal acrest in a cell galactic by 51 telephone for their principal disorders such as psoriasis and restenosis.
Polyglutamine repeat demain, bactingtin, atreghir, ataxin;
andragen receptor protoin, nounced programming discuso, antion
Huntington's discuso, dentatorubral pallidoluysian atrophy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Feptides binding to the DNA binding domain of transcription factor and inhibiting cell cycle progression, useful for the treatment of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wil, 2000 101806/48.
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                                                                                            Polyglutamine
                                                                                                                                            18-DEC-2001
                                                                                                                                                                                                                                      AMEICIBI standard, peptide,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cancer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26 JAN 2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                W0200044771-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       psoriasis; restenosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA binding, transcription factor, EDF, EDF-1, coll cycle; DF or tyan (a), transcription, ag gravit, p. 116 orthographic disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Peptide which binds to transcription factor E2F-1 DNA binding domain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Page 26; 42pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6 AA;
                                                                                                                                                                                                                                                                                                                                                         o,
                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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                                                                                                                                            (first entry)
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color, prod. Mr. 7.06.00;
cive 3; Mismanches 0;
                                                                                            domain binding peptide, QPB1-M7FD.
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[편 [편 [편]

DRPLA;

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RESULT 10
AAM45777
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Best Local s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence is a polygluramine repeat domain binding peptide. The postide is useful for treating a cell that contains and expresses a protein having an expended golygluramine region (e.g. buntingtin; atrophin 1. ataxin 1. 2. 6 or 7, or androgen receptor protein), or treating a neurodegenerative disease characterised by the presence of expanded polygluramine repeats, e.g. Huntington's disease, dentatorubral pailidoluysian atrophy (ORPLA), spinobulbar muscular atrophy, and spinocorobellar itrail types 1, 2, 3, 6 and 7
                                                                                                                                                                                              Antigen-binding, tumour, diagnosis, stress protein-peptide complex, SPPC, immunogenically cross-reactive, cancer; immunogenic cancer cell; cytostatio; varnino, timour specific immunogenic response inducer, astrocytoma, fibrish: "man, myvosarodma, lipusarodma, cligodendroglioma, ependymoma, medulichlastoma, primitive neural ectodermal tumour.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New polymortides which solor-ively himler expanded polyglutamine repeat domains, useful for treating neurodegenerative diseases, a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  spinobulbar muscular arrophy; spinover-bellar araxia; noorropic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 13; Page 14; Sopp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Huntington's disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Strittmatter WJ, Burke JR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unidentified.
                                                                                                                                                                                                                                                                                   Hill binding site monorposes meditering payride (mmp) #2048
                                                                                                                                                                                                                                                                                                                                                                          AAM45777 standard; Peptide; 7 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20-SEP-2001.
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            (NOVO ) NOVOPHARM BIOTECH INC
                                       08-DEC-1999;
                                                                    08-DEC-1999;
                                                                                                 08-JUN-2001
                                                                                                                            CA2290722-A1
                                                                                                                                                         Synthetic
                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                   25-00T-2001
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                                       ууСА-2290722.
                                                                    99CA-2290722
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50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 31; DB 22;
Pred. No. 7.8e+05;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 7;
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RESULT 11
AAR57399
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OC protein-peptide complexes (SPPC) associated with tumours that is conspectfically immunogenically cross-reactive with cell surface associated SPPCs specifically immunogenically cross-reactive with cell surface associated CC SPPCs specific to target cancer (TO. Also described is an isolated CC antigen binding fragment of an antibody that binds specifically to spons or a population of different spPCs consisting of immunogenic cancer cell CC curface associated SPPC of TO. (I) has sytuative activity and the consequence consequence in a consequence in a consequence of inducer. (I) is useful for treating 71 types of cancers or theorems in a consideration as astronymous, mediculobiasters, mysosarcoma, biposarcoma, collegedentroglioma, spendymoma, mediculobiasters, and primitive neural CC encornes. (I) is useful for diagnostic and palliative use, for detecting continuous continuous in an individual. AAM43/07 to AAM47109 represent populides which are used in the exemplification of the present invention.
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                              Disclosure; Page 12; 14pp; Japanese.
                                                                              A peptide and an adsorbing agent prepd. by immobilising it on a carrier useful for treatment of diseases related to ant: DNA
                                                                                                                                                                                                                                                                                                                                                                               Carrier; absorbing agent, treatment, anti-DNA antibody, immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Composition useful for treating and diagnosing marror, comprises stress protein-peptide complexes associated with tumor, and isolated antigen-binding fragments of an antibody that binds specifically to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kaplan HA, Maiti PK, Fast
Entwistle JM, MacDonald GC;
                                                                                                                                    WPI; 1994 260510/32
                                                                                                                                                                                                        30-SEF-1992;
                                                                                                                                                                                                                                                                                                             JF06102290-A
                                                                                                                                                                                                                                                                                                                                                                                                                 Peptide for treating diseases related to anti-DNA antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                      21-MAR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAR57399 standard; Protein; 8 AA
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                                                                                                                                                                                                                                          18-.TAM-1991;
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                                                                                                                                                                       (KUPS ) KUPARAY CO LTD
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nes 3; Conserva
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                                                                   and immune complexes
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The sequences given in AAR57386-413 are peptides which

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RESCULT 10

AAABO1440

CONTROL AAABO1

AAABO1440

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CONTROL AAAB
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Matches
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                                                                                                                                                                                                and inhibiting cell wile
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    Peptides which
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                                                                             Claim 4; Page
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     08-NOV-2000
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Tip, Phe or a peptide flajoust their injury flavosidues,

Tip, She, Ast will II.

Ed Y a bond or Arg. Cl. Arg. Lyr, Hir in a peptide fragrent consisting of 2 to residues, provided that at loast one X or Y are present;

OH or NH2; and
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                                                                        9: 4255.
bind to the DNA binding
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3; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            amino acid"
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Wo. 7.8e+05;
domain of transcription
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AAU93672
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Best Local Similarity
                                                                                                                                                                                                                            Newel compounds, useful for treating depressed neutrophic count
comprise peptide chains if approximately 6 to 40 amino acids in
that bind to granulocyte colony stimulating factor receptor -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    factor EDF and inhibit cell cycle progression may be useful as research agents to investigate the interestion between EDF and EP), it is a view to the form of principle progression. They old be used for inhibit approach on the cycle arrest in a cell particularly for inequality in the particularly for inequality in the consist.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3-COPE, granulacyte-filony stimulating factor receptor, cyth haemaropoietic growth factor; new rophil proliferation; AIDS, new rophil deficiency syndrom new rophil differentiation, acquired immunodeficiency syndrom chemicherapy induced meutographil, community acquired premion degreeced neutrophil count, immunestimulant.
                                                                                                                                                                                                         Claim 41; Page 67; 90pp; English
                                                                                                                                                                                                                                                                                                       Cwirla SE,
Schatz PJ;
                                                                                                                                                                                                                                                                                                                                                                                     TO THE COLL, COUNTY USD3046.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                              WELL ACOS SESESSIVE.
                                                                                                                                                                                                                                                                                                                                                             in 300 iosi, istologi seidell
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                                                                                                                                                                                                                                                                                                                                         9 AA;
                                                                                                                                                                                                                                                                                                                   Balu P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     colony stimulating factor receptor binding poptide #478.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLISCITATIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                         15 CUP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Perpetude;
                                                                                                                                                                                                                                                                                                                   Duffin DJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%, Score si, DM Li,
100.0%, Pred. No. 7.8e+05;
tive J. Mismatches G,
                                                                                                                                                                                                                                                                                                                  Piplani
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                                                                                                                                                                                                                                                                                                                   McEowen-Merrill
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Terror France
                                                                                                                                                                                                                                            in length
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RESULT 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best LC771 s
Matches 3
2\pm OH or WH2; and n\pm2.5 . These peptides may be immobilised on a carrier in the preparation
                                                                                                                                                              A = Trp. Phe or a peptide fragment consisting of 2 rasidues: B = Trp, Phe. Asn or Glu: As Trp, Phe. Asn or Glu: As Trp, Phe. Asn or Glu: As Trp, Phe. Asn or Asp. Glu, Arg. Lys, His or a peptide fra
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                     A peptide and an adsorbing agent prepd by immobilising it on carrier - useful for treatment of diseases related to anti-DNA \,
                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 12; 14pp; dapanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  JP06192290-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Peptide for treating diseases related to anti-DNA antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-MAR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAR57400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAR57400 standard; Prorein;
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                                                                                                                                                                                                                                                                          by the claimed generic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (KURS ) KURARAY CO LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30-SEP-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18-JAN-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12 JUL 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Carrier, absorbing agent, treatment, anti-DNA antib dy, immuse compos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4 WWGWNF 9
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                                                                                                                                                                                                                                                                                                         sequences given in AARETIRE 41% are peptides which are all revered
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1994-260510/32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                        Phe. Asm or Glu:
a bond or Asp, Glu, Arg, Lys,
consisting of 2-10 residues,
                                                                                                X or Y are present;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                               and immune complexes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        92JP 0261921
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100 CP;
                                                                                                                                                                                                                                                 H-X-(A-B)n-Y-Z
                                                                                                                                                                                                                                                                          formula:
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Pred. No. 7 Apros,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                               Tys, His or a peptide fragment
hes, provided that at least one
                                                                                                                                                                                                                                                                                                                                                                                                                                                           related to anti-DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
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AAW62149
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                            A method has been developed for identifying a ligand which mediates the CC biological activity of a target protein (T) by inhibiting the binding of (T) to a binding partner. The method comprises: (a) screening a first CC combinatorial library comprising first member ligands for binding to the CC screening a second library comprising first member ligands for binding to the CC screening a second library comprising second member ligands for the CC ability to inhibit the binding of one or more of the TBLs to the target CC protein, and so obtaining one or more inhibitory ligands; and (c) CC determining which of the inhibitory ligands can mediate a biological CC activity of the target protein. The present sequence represents a CC potential binding peptide for Haemophilus influence tyrocine tRNA CC synthetase from an example of the present influence tyrocine tRNA CC synthetase from an example of the present influence tyrocine tRNA CC synthetase from an example of the present influence tyrocine tRNA CC at target protein. It can be used to identify the biological activity of CC a target protein whose biological function is not known and perhaps CC at the determined directly. The method can also be used to identify the present introduced to identify of CC a target protein whose biological function is not known and perhaps CC mew inhibitory ligands of specific target proteins. The method provides thigh throughput screens which are essentially identical for similar and CC biochemically diverse targets.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DЬ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               absorbing agent which may be used in the treatment of diseases realated to anti-DNA antibodies and/or immune compex.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Haemophilus influenzae tyrosine tRNA synthetase binding poptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW62149;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW62149 standard, poptide, 11 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 5; Page 100; 143pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WFI; 1998-272389/24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            31-OCT-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                31-001-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Identifying ligands which mediate blooksgical activity of a protein by identifying target-binding ligands and screening a library for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fowlkes DM, Frelinger DA, Syde-Detayscher PD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (NOVA-) NOVALON PHARM CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ligands which inhibit target-binding ligand mediated activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Identification; ligand; biological activity; target-binding
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   screening, library; inhibitory ligand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 Similarity
3; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry
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Fred. No. 1.
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Ouery March

Best Local Similarity 50.0%; Pred. No. 2.1e+02;
Matches 1; Conservative 2; Mismatches 0; Indelc 0; Gaps 0;

Ouery March

Ouery Mismatches 0; Indelc 0; Gaps 0;

Ouery March

Ouery Mismatches

Ouery Mismatches

Ouery March

Ouery Mismatches

Ouery March

Ouery March